

**FIGURE 1**

CCAATCGCCCGGTGCGGTGGTGCAGGGTCTCGGGCTAGTCA**ATG**GCGTCCCCGTCTCGGAGAC  
 TGCAGACTAAACCAGTCATTACTTGTTTCAAGAGCGTTCTGCTAATCTACACTTTTATTTTC  
 TGGATCACTGGCGTTATCCTTCTTGCAAGTTGGCATTGGGGCAAGGTGAGCCTGGAGAATTA  
 CTTTTCTCTTTTAAATGAGAAGGCCACCAATGTCCCCTTCGTGCTCATTGCTACTGGTACCG  
 TCATTATTCTTTTGGGCACCTTTGGTTGTTTTGCTACCTGCCGAGCTTCTGCATGGATGCTA  
 AACTGTATGCAATGTTTCTGACTCTCGTTTTTTGGTCGAACTGGTCGCTGCCATCGTAGG  
 ATTTGTTTTCAGACATGAGATTAGAAGCAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGC  
 AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTGTCAT  
 TGTGTGGTGTCAACGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT  
 TCCTAAGAGTTGCTGTAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA  
 ATGAAGGTGTTTTATAAAGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA  
 ATTTCCCTTTGGAGTTGCTTGCTTCCAACCTGATTGGAATCTTCTCGCCTACTGCCWCTCTCG  
 TGCCATAACAAATAACCAGTATGAGATAGTG**TAA**CCCAATGTATCTGTGGGCCTATTCCCTCT  
 CTACCTTTAAGGACATTTAGGGTCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAAGT  
 ACAACACTACTTACTGATAGACCAAAAACTACACCAAGTAGGTTGATTCAATCAAGATGTAT  
 GTAGACCTAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT  
 TCAATCAAGATGTATGTTTGCTATGTTCTAAGTCCACCTTCTATCCCAATTCATGTTAGATCG  
 TTGAAACCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAAATGAAGT

**FIGURE 2**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902  
><subunit 1 of 1, 245 aa, 1 stop, 1 unknown  
><MW: -1, pI: 8.36, NX(S/T): 1  
MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGVSLNENYFSLLEKATNVPF  
VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGVFRHEIKNSFKN  
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDNTNYYSEKGFPSCKLEDCTPQ  
RDADKVNNEGCFIKVMTIIESEMGGVAGISFGVACFQLIGIFLAYCXSRITNNQYEIV

**Important features of the protein:****Signal peptide:**

amino acids 1-42

**Transmembrane domains:**

amino acids 19-42, 61-83, 92-114, 209-230,

**N-glycosylation site.**

amino acids 134-138

**Tyrosine kinase phosphorylation site.**

amino acids 160-168, 160-169

**N-myristoylation site.**

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 69-80, 211-222

**FIGURE 3**

CCCACGCGTCCGGCGCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCAAAA  
 GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGTCAGT  
 GCCACAGCCCCGACCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT  
 TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGAÇCGGACTGGG  
 GCCGGGGTAGGCTCTGAAAAGGGCCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA  
 GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCTTAGAAGAGGGT  
 GTTCCCTCTTTGCGGGGTCTCACCAGAAAGAGGTTCTTGGGGGTGCGCCTTCTGAGGAGGCT  
 GCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCTGTAGTTGATAATGTTG  
 GGAATAAGCTCTGCAACTTTCTTTGGCATTGAGTTGTTAAAAACAAATAGGATGCAAAATTC  
 TCAACTCCAGGTTATGAAAAAGTACTTGGAAAACTGAAAACTACCTAAATGATCGTCTTTG  
 GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG  
 CACATAGCCCACTTCTTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG  
 CCGAGATGACAGTGAACAGATGACAGTGTTGACACCCAACAGCAACAGGCCGAGAACAGTG  
 CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCTGTTGCGCCACCAAGGAGGGGG  
 CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT  
 GGCAGTAATACGGACTCTTGTAGATAAGTAAAGTATCTGACTCACGGTCACCTCCAGTGAAT  
 GAAAAGTGTTCTGCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG  
 CCAAGCCTTGTGCTCAGAGGCAAGGAGAATATTTAATGCTCCGCTGATGGCAGAGTAAA  
 TGATAAGATTTGATGTTTTGCTTGCTGTCATCTACTTTGCTCTGGAATGTCTAAATGTTTC  
 TGTAGCAGAAAACACGATAAGCTATGATCTTTATTAGAG



GGACACGAGGCGCTGTCCACCCGGGGCGTGGGAGTGAGGTACCAGATTACGCCCATTTGGCC  
CCGACGCCCTCTGTTCGGAATCCGGGTGCTGCGGATTGAGGTCCGGTTCCTAACGGACTG  
CAACATGGAGGAAGGCGGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT  
CAGGTGCCTGGGGCATGCAAAATGTGGGTGACCTTCGTCTCAGGCTTCCTGCTTTTCCGAAGC  
CTTCCCGACATACTTCGGACTAGTGCAGAGCAAACCTCTCCCTTCTACTTCCACATCTC  
CATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCA  
CATTCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCTCTGAGCCTTACGCTGGCCATGTCAAC  
GCCCGCTGGCTGGAACCCCGCACACAGCTGCCATGTGGGCCTGCAAAACCGTGGAGAAGGA  
GCGAGGCTGGGTGGGAGGTACCAGGCAGCCACCAGGGTCCCGATCCCTACCGCCAGCTGC  
GAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTTCTTCCGCTACCATGGGCTGTCC  
TCTCTTTGCAATCTGGGCTGCGTCTGAGCAATGGGCTCTGTCTCGCTGGCCTTGCCCTGGA  
AATAAGGAGCCTCTAGCATGGGCCTGCAATGCTAATAAATGCTTTCCAGAAATGAAAAAA  
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**FIGURE 6**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107

<subunit 1 of 1, 231 aa, 1 stop

<NX(S/T): 0

MEEGNGLGLIKMVHLLVLSGAWGMQMWVTFVSGFLLFRSLPRHTFGLVQSKLFPFYFHISM  
GCAFINLCILASQHAWAQLTFWEASQLYLLFLSLTLATVNARWLEPRTTAAMWALQTVEKER  
GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFERYHGLSSLCNLGCVLSNGLCLAGLALEIRSL

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 86-103, 60-75

**Casein kinase II phosphorylation site.**

amino acids 82-86

**Tyrosine kinase phosphorylation site.**

amino acids 144-151

**N-myristoylation site.**

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 54-65

**G-protein coupled receptors proteins.**

amino acids 44-85

**FIGURE 7**

AATTCAGATTTTAAAGCCATTCTGCAGTGGAAATTTTCATGAACTAGCAAGAGGACACCATCTT  
 CTGTATTATACAAGAAAGGAGTGTACCTATCACACACAGGGGAAAA**ATG**CTCTTTTGGGT  
 GCTAGGCCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAACTAAAGATTGAAG  
 ACATCACTGATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCC  
 AGAATTTTGATAAAAAGGGATTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAAC  
 AGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAG  
 AGAATGTCAAGAGGACTGCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGT  
 CTGATCAATAATGTGGTGTCCCGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGA  
 CTACAGAGAACCTATTGAAGTGAACCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTC  
 CTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCAGTGTGGAGGTCGCCCTTGCA  
 ATCGTTGGAGGGGGCTATACTCCATCCAAATATGCAGTGGAAAGGTTTCAATGACAGCTTAAG  
 ACGGGACATGAAAGCTTTTGGTGTGCACGTCTCATGCATTGAACAGGATTGTTCAAAACAA  
 ACTTGGCAGATCCAGTAAAGGTAATTGAAAAAACTCGCCATTTGGGAGCAGCTGTCTCCA  
 GACATCAACAACAATATGGAGAAGGTTACATTGAAAAAAGTCTAGACAACTGAAAGGCAA  
 TAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA  
 GTCTCTCCCTAAGACTCATTATGCCGCTGGAAGATGCCAAAATTTTCTGGATACCTCTG  
 TCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA  
 TCCCAAGGCAGT**GTGA**CTCAGCTAACACAAATGTCTCCTCCAGGCTATGAAATTGGCCGAT  
 TTCAAGAACACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACTCATTTAGA  
 TCGTGCTTATTGGATTGCAAAAGGGAGTCCACCATCGCTGGTGGTATCCAGGGTCCCTG  
 CTAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCTGCCCTGT  
 ATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCAITCAAATG  
 ATCTTTACCGTGGCTGCCCCATGCTTATGGTCCCAGCATTTACAGTAACTGTGAATGTT  
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 AAAAAAAAAAAAAAAAAAAAA

**FIGURE 8**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406
><subunit 1 of 1, 319 aa, 1 stop
><MW: 35227, pI: 8.97, NX(S/T): 3
MLFWVLGLLILCGFLWTRKGLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLT
ESGSTALKAETSERLRTVLLDVTDPENVKRTAQWVNQVGEKGLWGLINNAGVPGVLAPTDW
LTLEDYREFIEVNLFG LISVTLNMLPLVKKAGRVINVSSVGGRLAIVGGGYTPSKYAVEGF
NDSLRRDMKAFGVHVSCEI EPLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEGYIEKSLD
KLKGNKSYVNMDLSPVVECDHALTSLFFKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK
AELANPKAV
```

**Important features of the protein:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 136-152

**N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

**Glycosaminoglycan attachment site.**

amino acids 39-42

**N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212



**FIGURE 9**

GCGGGCTGTTGACGGCGCTGCG**ATGG**GCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT  
 CCTCTCAGTCGGACTTCTTGACGCCGCCAGTGGCGGGGGCCCTTGGGGCGTGCACCACCT  
 GTAGTCATGTACCCACGCCGCCGCCGCCCTCATCGGGACTTCATCTCGGTGACGCTGAG  
 CTTTGGCGAGAGCTATGACACAGCAAGAGTTGGCGCGCGCGCTGCTGCTGGAGAAATGGA  
 AGCAACTGTCCGAGATTGACGCGGAATATGATTCTCTCTCCTTGCCTTTCTGCTTTTCTGT  
 GGACTCCTCTTCTACATCACTTGGCTGACCATTGGAAAGCTCTGGCTTTCAGGCTAGAGGA  
 AGAGCAGAAGATGAGGCCAGAAATTGCTGGGTAAAACCAGCAATCCACCCGTCTTACCAG  
 CTCTTCAGAAGGGCGGACACCACCTGAGAACTTACCTGAGATTTCGTACAGAAAGACACAA  
 AGACACATCCAGCGGGGACCACCTCACCTGCAGATTAGACCCCCAAGCCAAGACCTGAAGGA  
 TGGGACCCAGGAGGAGGCCACAAAAGGCAAGAGCCCTGTGGATCCCCGCCCGGAAGGAG  
 ATCCGCAGAGGACAGTCATCAGCTGGAGGGGAGCGGTGATCGAGCCTGAGCAGGGCACCGAG  
 CTCCCTTCAAGAAGAGCAGAAGTGGCCACCAAGCCTCCCTGCCACCGGCCAGGACACAGGG  
 CACACCACTGCATCTGAACATATCGCCAGAAGGGCGTGATTGACGCTTCTCTGCATGCATGGA  
 AAGGATACCCAAAGTTTTCATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCCTTCAGT  
 GAGTGGTTTGGCCTCGGTCTCACACTGATCGACGCGCTGGACACCATGTGGATCTTTGGGTCT  
 GAGGAAAGAAATTTGAGGAAGCCAGGAAGTGGGTGTGCGAAGAAGTTACACTTTGAAAAGGACG  
 TGGAGCTCAACCTGTTTGTAGAGCACGATCCGCATCCTGGGGGGGCTCCTGAGTGCCCTACCAC  
 CTGTCTGGGGACAGCCTTCTTCTGAGGAAAGCTGAGGATTTTGGAAATCGGCTAATGCCTGC  
 CTTCAAGACACCATCCAAGATTCTTACTCGGATGTGAACATCGGTACTGGAGTTGCCACC  
 CGCCACGGTGGACTCCGACAGCACTGTGGCCGAGGTGACCAGCATCAGCTGGAGTTCCGG  
 GAGCTCTCCCGTCTCACAGGGGATAAGAAGTTTCAGGAGGCACTGGAGAAGGTGACACAGCA  
 CATCCACGGCCTGTCTGGGAAGAAGGATGGGCTGGTGCCCATGTTTCATCAATACCCACAGTG  
 GCCTTTTACCCACCTGGGCGTATTACGCTGGGCGCCAGGGCCGACAGCTACTATGAGTAC  
 CTGCTGAAGCAGTGGATCCAGGGCGGGGAAGCAGGAGACACAGCTGCTGGAAGACTACGTGGA  
 AGCCATCGAGGGTGTGAGAAGCAGCACTGCTGCGGCCTCCGAGCCAGTAAGCTCACTTTTG  
 TGGGGGAGCTTGCCACGGGCCGCTTCAGTGCCAAAGATGGACCACCTGGTGTGCTTCTCGCCA  
 GGGACGCTGGCTTGGGCGCTTACCACGGCCTGCCCGCCAGCCACATGGAGCTGGGCCAGGA  
 GCTCATGGAGACTTGTACCAGATGAACCGGCAGATGGAGACGGGGCTGAGTCCCGAGATCG  
 TGCATTTCAACCTTTACCCCCAGCCGGGCCGTGGGACGTGGAGGTCAAGCCAGCAGACAGG  
 CACAACCTGCTGCGGCCAGAGACCGTGGAGAGCCTGTTTACCTGTACCGCCTCACAGGGGA  
 CCGCAATACCAGGACTGGGCTGGGAGATTCTGCAGAGCTTCAGCCGATTACACGGGTCC  
 CCTCGGCTGGCTATTCTTCCATCAACAATGTCCAGGATCTCAGAAGCCCCAGCCTAGGGAC  
 AAGATGGAGAGCTTCTTCTGGGGGAGACGCTCAAGTATCTGTTCTTGCTCTTCTCCGATGA  
 CCCAAACCTGCTCAGCCTGGACGCTACGTGTTCAACACCGAAGCCCAACCCTCTGCCATATC  
 GGACCCCTGGCT**AGG**GTGGATGGCTGCTGGTGTGGGACTTCGGGTGGGCGAGGCAAGCTTG  
 CTGGGTCTGTGGCATTTTTCCAAGGGCCCACGTAGCACCGGCAACCGCCAAGTGGCCAGGCT  
 CTGAATGGCTCTGGGCTCCTCCTCGTCTGTGTTAATCAGGACACCGTGAGGACAAGTGA  
 GGCCCTCAGTCTTGGTGTGATGCGGGGTGGGCTGGGCCGCTGGAGCCTCCGCTGCTTCTC  
 CAGAAGACACGAATCATGATCAGCATGCTGAGGCTGAGCAGGTCTCTGTGGGCCGACCA  
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 CTCGAGGCGCTCAGGCTCAGGGCTGGCTCTGGTGTTCACAGCTGAGCTCAGGATCCTC  
 CTGGCGCGCCCGCAGGGGGCTGGAGGGCTGGACGGCAAGTCCGCTTACGTACAGCGGCCCT  
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**FIGURE 10**

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IAGLKPANFPVLPAPQKADTDPENLPEISSQKTQRHIQRGFPHLQIRPPSQDLKDGTEQEEAT
KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTELPSRRAEVPTKPPLPPARTQGTVPVHLNY
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGGLGLTLIDALDTMWILGLRKEFEEA
RKWVSKKLHFEKDVVDNLFESTIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI
PYSVDNIGTGVAHPPRWTSDSTVAEVTISIQLEFRELSRLTGDKKFQEAVEKVTQHIHGLSGK
KDGLVPMFINTHSGLFTHLGVFTLGARADSYEYLLKQWIQGGKQETQLEDYVEAIEGVRT
HLLRRHSEPSKLTFFVGEAHGRFSAKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ
MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNLLRPETVESLFYLYRVTGDRKYQDWG
WEILQSFSRFRTRVPSSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLFSDDPNLLSLD
AYVFNTEAHPLPIWTPA
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**Important features of the protein:****Transmembrane domain:**

amino acids 21-40 and 84-105 (type II)

**FIGURE 11**

GGCGCCGCGTAGGCCCGGGAGGCCGGGCCGGGCTGCGAGCGCCTGCCCATGCGCCGC  
CGCCTCTCCGCACG**ATG**TCCCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGC  
AGGTCCGGGTTGCTCTCCGGCGGCCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTCTGTGGC  
CTGCCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG  
CCCCGGGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCTGCCCCCAGAG  
CCGCCCTTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCACCGCTGGCAGTGCTGGT  
GCCCTTCCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCACATGCGCGCTTCCTGA  
GCAGGAAGAAGATCCGGCACCACATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAAC  
CGGGCAGCGCTCATCAACGTGGGCTTCTTGAGAGCAGCAACAGCACGGACTACATTGCCAT  
GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGC  
CCTTCCACGTGGCCTCCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTCGGCGGC  
ATCCTGCTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGG  
CTGGGGCCCGCAGGACGACGAGTTCTACCGGCGCATTAAGGGAGCTGGGCTCCAGCTTTTCC  
GCCCTCGGGAATCACAACTGGGTACAAGACATTTGCCACCTGCATGACCCAGCTGGCGG  
AAGAGGGACACAGAAGCGCATCGCAGCTCAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGG  
AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGCGGGGGCC  
CCTGCACTGTCTCAACATCATGTTGGACTGTGACAAGACCGCCACACCTGGTGACATTC  
AGC**TGA**AGTGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGA  
CAAGGCCTCAGGTCGTGGGCCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA  
AGCTACGCAATTGCAGCCACCCGGCCGCCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGG  
GTGCTTGGGACGCTGCTTGCCATGCACAGTGATCAGAGAGAGGCTGGGGTGTGTCTGTCCG  
GGACCCCCCTGCCTTCTGTCTCACCTACTCTGACCTCCTTCACGTGCCAGGCCTGTGGG  
TAGTGGGAGGGCTGAACAGGACAACCTCTCATCACCTACTCTGACCTCCTTCACGTGCC  
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**FIGURE 12**

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MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLFVACL1SLGFFSLLWLQLSCSGDVARAVR
GQGQETSGPPRACPPPEPPPEHWEEDASWGPHRLAVLV2PFRRERFEELLVFVPHMRRFLSRKKI
RHHIYVLNQVDHFRFNRAALINVGFLESSNSTDYIAMHDVDLLPLNEELDYG3GFPEAGPFHVA
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDD4EFYRRIKGAGLQLFRPSGI
TTGYKTFRHLHDPAWRRKRDQKRIAAQKQE5QFKVDREGGLNTVKYHVASRTALSVGGAPCTVL
NIMLDCDKTATPWCTFS
```

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 29-49 (type II)

**N-glycosylation site.**

amino acids 154-158

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 27-31

**Tyrosine kinase phosphorylation site.**

amino acids 226-233

**N-myristoylation site.**

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

**FIGURE 13**

CAATGTTTGCCTATCCACCTCCCCCAAGCCCCTTTACCT**ATG**CTGCTGCTAACGCTGCTGCT  
 GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCAGAAAGTCT  
 CTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTC  
 CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCAGCCCCGTGGGGAAGGGGAGAAAGT  
 GGGGATGGC**TAA**GAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGG  
 GCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGC  
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 AAATATGTCTTTATAATAAACAGTTAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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MLLLTLLLLLLLLLKSGSCLWGLVGAQKVSSATDAPIRDWAFPPSPFLCLLPHRPAMTCSQAQ
PRGEGEKVGDG
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Important features:

Signal peptide:

amino acids 1-15

**Growth factor and cytokines receptors family:**

amino acids 3-18

**FIGURE 15**

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGAGCGGACAAAG  
GAGCATGTCCGCGCCGGGGAGGCCCGCTCCTCCGGCCGCCATAAAGGCTCCGGTCGCCGCTGG  
GCCCGCGCCGCGCTCCTGCCCGCCGGGCTCCGGGCGGCCCGCTAGGCCAGTGCGCCGCCG  
CTCGCCCCGACGCCCGGCCGAGC**ATG**GAGCCACCCGGACGCCGGCGGGCGGCCGCGCA  
GCCGCCGCTGTTGCTGCCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGAGCGCGCGCG  
CGCGCGCGCGCGCGCGGCTCGCCCGCGCTGCAAGCACGATGGCGGCCGCCGAGGGCTGGC  
AGGGCGCGGGCGCGCCGAGGGCAAGTGGTGTGCAGCAGCCTGGAACCTCGCGCAGGTCTCT  
GCCCCAGATACCTCTGCCAACCGCACGGTCAACCCTGATTCTGAGTAACAATAAGATATCCG  
AGCTGAAGAATGGCTCATTTTCTGGGTAAAGTCTCCTTGAAGATTGGACCTCCGAAACAAT  
CTTTATAGTAGTATAGATCCAGGTGCCTTCTGGGGACTGTCTCTCTAAAAAGATTGGATCT  
GACAAACAATCGAATAGGATGTCTGAATGCAGACATATTTTCGAGGACTCACCATCTGGTTC  
GGCTAAACCTTTTCGGGGAATTTGTTTTCTTCATTATCTCAAGGAACCTTTTGATTATCTTGGC  
TCATTACGCTCTTTGGAATTCAGACTGAGTATCTTTTGTGTGACTGTAACATACTGTGGAT  
GCATCGCTGGGTAAGGAGAACAATCACGGTACGGGATACCGAGTGTGTTTATCCTAAGT  
CACTGCAGGCCCAACAGTCAACAGCGTGAAGCAGGAGCTGTTGACATGCGACCCCTCCGCTT  
GAATGCGCTCTTTCTACATGACTCCATCTCATCGCCAAGTTGTGTTTGAAGGAGACAGCCCT  
TCCCTTCCAGTGCATGGCTTCATATATTGATCAGGACATGCAAGTGGTTGTGATCAGGATG  
GGAGAATAGTTGAACCGATGAATCGCAAGGTATTTTGTGTGAAGAAGACATGATTCACAAC  
TGCTCCTTGATTGCAAGTGCCCTAACCATTTCTAATATTAGGCTGGATCTACTGGAAATTG  
GGGCTGTGATGTCAGACCAACGTGGGAATAATACGAGGACTGTGGATATTGTGGTATTAG  
AGAGTTCTGCACAGTACTGTCTCCAGAGAGGGTGGTAAACAACAAAGGTGACTTCAGATGG  
CCCAGCAATTGGCAGCAGTACTGCATATCTGCAGTGTACGCGGAACACCCATGGCAGTGG  
GATATATCCCGAAACCCACAGGATGAGAGAAAAGCTTGGCGCAGATGTGATAGAGTGGCT  
TTTGGGCAGATGATGATTATTTCTCGCTGTGATGCAAAATGATGTCACTAGAGTTCTTTAT  
ATGTTTAATCAGATGCCCTCAATCTTACCAATGCCGTGGCAACAGCTCGACAGTTACTGGC  
TTACACTGTGGAAGCAGCCAACCTTTTCTGACAAAATGGATGTTATATTGTGGCGAAGATGA  
TTGAAAAATTTGAAGATTATACCAAGGAGGAAAAATCAAAAGACATAGTGACGTGATGGTT  
GACATTCGAAGTAACATCATGTTGGCTGATGAACGTGTCTGTGGCTGGCGCAGAGGGAAGC  
TAAAGCCTGCAGTAGGATTGTGCAGTGTCTTACGCGCATTGCTACCTACCGGTATCCCGGTG  
GAGCTCACGTTTTATTCAACATATTCACCCAATATTGCTCTGGAAGCTTATGTCACTAAGTCT  
ACTGGCTTACGCGGATGACCTGTACCGTGTTCAGAAAATGGCAGCCTCTGTATCGTACAGG  
ACTTTCGGATTATGGGAGGCGGGATCCAGAGGGAACCTGGATAAGCAGCTGAGCTTTAAGT  
GCAATGTTTCAAATACATTTTCGAGTCTGGCACTAAAGGTATGTTACATCTGCAACATTTT  
AAGACTATTTACAGT**TAA**ATTAGAATGCTCCAATGTTCTGCTTCGCAAAAATAACCTTATTA  
AAAGATTTTTTTTTGAGGAAGATAGGTATTATTGCTTTTGTCTACTGTTTAAAGAAAACTA  
ACCAGGAAGAACTGCATTACGACTTTCAAGGGCCCTAGGCATTTTTGCTTTTGATTCCCTTT  
CTTCACTAAAAATATCAGAAATTACATTTTATAACTGCAGTGGTATAAATGCAAAATATACAT  
ATTTACATGTGAAAAAATTTTATTGACTTAAAGTTTATTTATTTGTTTTTGTCTCCCT  
GATTTTAAGACAATAAGATGTTTTCATGGGCCCTAAAGATATCATGAGCCTTTGGCACTGC  
GCCTGCCAAGCCTAGTGGAGAAGTCAACCTGAGACCAGGTGTTTTAATCAAGCAAGCTGTAT  
ATCAAAATTTTGGCGAAAAACACAATATGTCAATATCTTTTTTAAAAAAGATATTTCA  
TTGAAGCAAGCAAAATGAAGCATTTTACTGATTTTTTAAATTTGGTGCTTTAGATATATTT  
GACTACACTGTTTGAAGCAATAAGAGGAGGCACAACCTCCAGCACCTTATGGAACACATTT  
TTTTTCACTTAGCTTCTGTGGGCATGTGTAATTGTATTCTCTCGCGTTTTTAACTCTACAG  
TACTTTATTTCTGTCTGTGCCCTCAATAATATCAACAACATATTCAGTCACTTTAATGGC  
TGCATAATAACTGATCCAAAGGTGTAGGTGTTTGTAGTTAGTGAGCATCTCAATTAATA  
TTGAATGAATGAACGAAAAAAAAAAAAAAAAA

**FIGURE 16**

MEPPGRRRRGRAQPPLLLPLSLLALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK  
 VVCSLSLELAQVLPDPTLPNRTVTLLSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA  
 FWGLSSSLKRDLDTNNRIGCLNADIFRGLTNLVRNLNSGNLFSSLSQGTFDYLASLRSLFQT  
 EYLLCDCNILMWHRWVKEKNITVRDTRCVYPKSLQAQPVTVGVKQELLTCDPPELPSFYMTF  
 SHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRIVETDESQGIFVEKNMIHNCSLIASALT  
 ISNIQAGSTGNWGCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGFWRWPRTLAGITA  
 YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQMPNLN  
 TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDMVDIASNIMLA  
 DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSFNIALEAYVIKSTGFTGMTCT  
 VFQKVAASDRTGLSDYGRDPPEGNLDKQLSFKCNVSNTFSSLALKVCYILQSFKTIYS

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 13-40 (type II)

**N-glycosylation site.**

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,  
 433-437, 453-457, 592-596

**N-myristoylation site.**

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,  
 57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,  
 384-390, 403-409, 554-560



**FIGURE 17**

GCGTGGGGGATGTCTAGGAGCTCGAAGGTGGTGTGGGCCCTCTCGGTGCTGCTGACGGCGGCC  
 ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT  
 CAGAGACATTGAGAGGCAAATTGCGAAAAAGAAAACATTCGTCTTTTGGGAGAACAGATTA  
 TTTTGACTIONGAGCAACTTGAAGCAGAAAAGAGAGAAGATGTTATTGGCAAAGGATCTCAAAA  
 TCATTGACTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTGAT  
 GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAAACTTGATCA  
 AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGA  
 GTGTGGGCAGACACTTTTGAAGACTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG  
 TCACGTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA  
 TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA  
 TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGAGGGGAGAGACGCTCCTGATCGTCGAATCC

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**FIGURE 18**

MSRSSKVVLGLSVLLTAATVAGVHVKKQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT  
EQLEAEREKMLLAKGSQKS

**Signal peptide:**

amino acids 1-21

1 MS  
2 RS  
3 SK  
4 VV  
5 LG  
6 LS  
7 VV  
8 LL  
9 TA  
10 AT  
11 VA  
12 GV  
13 HV  
14 KK  
15 QW  
16 DQ  
17 QR  
18 LR  
19 RD  
20 GV  
21 IR  
22 DI  
23 ER  
24 QI  
25 RK  
26 KE  
27 NI  
28 RL  
29 LG  
30 EQ  
31 II  
32 LT  
33 EQ  
34 LE  
35 AE  
36 RE  
37 KM  
38 LL  
39 AK  
40 GS  
41 SQ  
42 KS

**FIGURE 19**

CTGTCGCTCTTTGCTTCAGCCGAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTC  
 CAAGTGTGGCTTAATCCGCTCTCCACCACCAGATCTTTCTCCGTGGATTCTCTGCTAAGACC  
 GCTGCC**ATG**CCAGTGACGGTAACCCGACCACCATCACAACCACCACGACGTCATCTTCGGG  
 CCTGGGGTCCCCCATGATCGTGGGGTCCCTCGGGCCCTGACACAGCCCCTGGGTCTCCTTCGC  
 CTGCTGCAGCTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGCTAGCGTGGGCGCTGGAC  
 GGGGTCCATGGGCACTGGTCCATGTTACCTGGTGTCTTCTGCTTCTCCGTGACCCTGATCA  
 TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCGCTTCCCCCTGTCTTGCGCAACTTCCCC  
 ATCACCTTCGCCTGCTATGCGGCCCTCTTCTGCTCTCGGCCTCCATCATCTACCCACCAC  
 CTATGTCCAGTTCCTGTCCACGGCCGTTGCGGGGACCACGCCATCGCCGCCACCTTCTTCT  
 CCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCCTGGACCCGGGCCCGGCCCGCGAG  
 ATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGTGCTGGAGACCTTCGTTGCCTG  
 CATCATCTTCGCGTTATCAGCGACCCCAACCTGTACCAGCACCAGCCGGCCCTGGAGTGGT  
 GCGTGGCGGTGTACGCCATCTGCTTATCCTAGCGGCCATCGCCATCCTGCTGAACCTGGGG  
 GAGTGCACCAACGTGCTACCATCCCCCTCCCGAGCTTCTGTGCGGGCTGGCCTTGTGTGTC  
 TGTCTCTCTATGCCACCGCCCTTGTCTCTGCCCCCTTACAGTTCGATGAGAAGTATG  
 GCGGCCACGCTCGCGCTCGAGAGATGTAAGCTGCAGCCGACCCATGCCTACTACGTGTGT  
 GCCTGGGACCGCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTATGTGGC  
 TGACCTGGTGCACCTCTGCCACCTGGTTTTTGTCAAGGTCT**TAA**GACTCTCCAAGAGGCTCC  
 CGTTCCCTCTCCAACCTCTTTGTTCTTCTTGCCGAGTTTTCTTTATGGAGTACTTCTTTCC  
 TCCGCTTTTCTGTGTTTCTCTTCTTCTCCCCCTCCCCTCCCACCTTTTTCTTTCTTCC  
 CAATTCCTTGCACTCTAACAGTTCTTGGATGCATCTTCTTCTTCTTCTTCTTCTGCTGT  
 TTCCTTCTGTGTGTTTTGTTGCCACATCCTGTTTACCCCTGAGCTGTTTCTCTTTTT  
 CTTTTCTTTCTTTTTTTTTTTTTTTTAAAGCGATTCTCACTCTGTGGCCAGGCTGGAG  
 TGCAGTGGTGCATCTCAGCTCACTGCAACCCCCGCTCCTGGGTTCAGCGATTCTCCTCC  
 CCCAGCCTCCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGACCCAGCCTGTTTCTCTTT  
 TTCCACTCTTCTTTTTTCTCATCTCTTTTCTGGGTGCGCTGTGCGCTTTCTTATCTGCCTGT  
 TTTGCAAGCACCTTCTCCTGTGCTCTTGGGAGCCCTGAGACTTCTTCTCTCCTTGCTCCA  
 CCCACCTCCAAAGGTGCTGAGCTCACATCCACACCCTTGACCGCTCCATGCCACAGCCCC  
 CCAAGGGGCCCATTGCCAAAGCATGCCTGCCACCCTCGCTGTGCCTTAGTCAGTGTGTAC  
 GTGTGTGTGTGTGTGTTTTGGGGGTGGGGGTGGGTAGCTGGGATTGGGCCCTCTTCT  
 CCCAGTGGAGGAAGGTGCAGTGTACTTCCCTTTAAATTAAAAACATATATATATATAT  
 ATTTGGAGGTCAGTAATTTCCAAATGGGCGGGAGGCATTAAGCACCGACCTGGGTCCCTAGG  
 CCCCCTGGCACTCAGCCTTGCCAGAGATTGGCTCCAGAAATTTTGCCAGGCTTACAGAACAC  
 CCACTGCCTAGAGGCCATCTTAAAGGAAGCAGGGGCTGGATGCCTTTCATCCCACTATTCT  
 CTGTGGTATGAAAAAG

**FIGURE 20**

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVTRTTITTTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCFSVTLIIILIVELCGLQARFPLSWRNFPITFACYAALFCLSASIIYPTTY
VQFLSHGRSRDHAIAATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLETFVACI
IFAFISDPNLYQHQPAALEWCVAVYAICFILAAIAILLNLGECTNVLPPIPFPSFLSGLALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD
LVHSAHLVFVKV

```

**Important features:****Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,  
205-226, 235-255 and 294-312

**N-glycosylation site.**

amino acids 66-69

**Glycosaminoglycan attachment site.**

amino acids 18-21

[illegible]

**FIGURE 22**

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSPFSHPKVHMDPNYCHPSTSLHLCS  
 LAWSFTRLLHPPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALSAFSSY  
 SDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG  
 PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVSPDTLCSSLCSLEDGLLGSPARLASQLLGDE  
 LLLAKLPPRESAFRSLGPLEAQDSLNSPLTESCLSPAEEEPAPCKDCQPLCPPLTGSWER  
 QRQASDLASSGVVSLDEDEAEPEEQ

**Signal peptide:**

amino acids 1-15

**Casein kinase II phosphorylation site.**

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,  
 285-289, 324-328

**Tyrosine kinase phosphorylation site.**

amino acids 44-52

**N-myristoylation site.**

amino acids 17-23, 26-32, 173-179

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 11-22

**FIGURE 23**

GGTTCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTTGTTCCTCT  
 GGCACCCCTCTGCTCAGTGCACATTTGTACACTTAACCCATCTGTTTCTCTAATGCACGA  
 CAGATTCCTTTACAGACAGGACAACCTGTGATATTTAGTTCCTGATTGTAAATACCTCCTAAG  
 CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTTCTTCTATCTGCAAAATGGGCATAA  
 TACAATCTATTCTTGCACATCAAGGGATTGTTATTCCTTTAAAAAAAACCAATACCAAAG  
 AAGCCTACAATGTTGGCCTTAGCCAAAATTCTGTTGATTTCAACGTTGTTTTATTCACTTCT  
 ATCGGGGAGCCATGGAAGAAAATCAAGACATAAACACAACACAGAACATTGCAGAAGTTT  
 TTAACAATGGAATAAACCTATTTCTTTGGAAGTGAAGCAAACCTTAACTCAGATAAA  
 GAAATATAACCCTCAAATCTCAAGCGAGTCATTCCTCTCTTGAATCTACCCAACAA  
 CAGCCACGGAATAACAGATTTCTCCAGTAACCTCATCAGCAGAGCATTCTTTGGGCAGTCTAA  
 AACCACATCTACCATTTCCACAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAAAGTGCT  
 TGGAAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCAGATCCCAATGCTACACC  
 TGCTCTGTCTTCAGAAAACCTCACTTGGTCTTTGGTCAATGACACCGTGAACCTCCTGATA  
 ACAGTTCCATTACAGTTAGCATCCTCTCTTCAGAACCACTTCTCCATCTGTGACCCCTTG  
 ATAGTGGAACCAAGTGATGGCTTACCACAAACAGTGATAGCTTCACTGGGTTTACCCCTTA  
 TCAAGAAAAAACCTCTACAGCCTACCTTAAATTCACCAATAATCAAACCTTTTCCAA  
 ATACGTGAGATCCCCAAAAAGAAAATAGAAATACAGGAATAGTATTGCGGGCCATTTTAGGT  
 GCTATTCTGGGTGTCTCATTGCTTACTCTTGTGGGCTACTTGTGTGTGGAAGGAAAAC  
 GGATTCTATTTCCCATCGGCGACTTTATGACGACAGAAATGAACAGTTCTGCGATTAGACA  
 ATGCACCGGAACCTTATGATGTGAGTTTTTGGGAATTCTAGCTACTACAATCCAACCTTTGAAT  
 GATTGAGCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCTCTATGGATGACATACC  
 TCCACTTCTGTACTTCTGTATAGAACTAACAGCAAAAAGGCGTTAAACAGCAAGTGTCATCTA  
 CATCTAGCCTTTTGACAAATTCATCTTTCAAAGGTTACACAAAATTAAGTGTACGTTGGAT  
 TTTGTCAAGGAGAATCATAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT  
 CCAAAGGTTTTCTTCTTACAATTTTGGCCATCCTGAGGCATTTACTAAGTAGCCCTTAATT  
 TGTATTTTAGTAGATTTTCTTAGTAGAAAAATTTGTGGAATCAGATAAACTAAAAGATT  
 TCACCATTCAGCCCTGCTCATAACTAAATAATAAAATTTATCCACCAAAAAATCTAAA  
 ACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATTCAAGATTGCAT  
 TTTCTTAAATGAAAATTGAAAGGTGCTTTTTAAAGAAAATTTGACTTAAAGCTAAAAGAG  
 GACATAGCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTC  
 TAGTACGTTATAATTTCTAGATCAGCACACATGATCAGCCCACTGAGTTATGAAGCTGA  
 CAATGACTGCATTCAACGGGGCCATGGCAGGAAAGCTGACCCATACCAGGAAAGTAATAGCT  
 CTTTTAAAGTCTTCAAAGTTTTGGGAATTTTAACTTGTCTTAATATATCTTAGGCTTCAA  
 TTATTTGGGTGCCTTAAAACCTCAATGAGAATCATGGT

**FIGURE 24**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732
><subunit 1 of 1, 334 aa, 1 stop
><MW: 36294, pI: 4.98, NX(S/T): 13
MLALAKILLISTLFYSLLSGSHGKENQDINTTQNIAEVFKTMENKPISLESEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNA
PIADEDLLPISAHPNATPALSSNFVWTLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLFNPTSDPQKENRNTGIVFGAILGAIL
GVSLTLVGILLCGKRKTDTSFHRRLYDDRNEFVLRLDNAPEPYDVSVGNSSYYNPTLNDSA
MPESEENARDGIPMDIPPLRTSV
```

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 235-262

**N-glycosylation site.**amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,  
163-167, 218-222, 225-229, 298-302, 307-311



**FIGURE 25**

AACAGGATCTCCTCTTGCAGTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC  
 AGCCCGAAGATTCACT**ATG**GTGAAAAATCGCCTTCAATACCCCTACCGCGGTGCAAAAGGAGG  
 AGGCGCGGCAAGACGTGGAGGCCCTCCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC  
 AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT  
 CTTAGGCCTTTCATTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATTTACAAGTACT  
 TCATGCCCAAGAGCACCATTACCGTGGAGAGATGTGCTTTTTTGATTCTGAGGATCCTGCA  
 AATCCCTTCGTGGAGGAGAGCCTAATTCCTGCCTGTGACTGAGGAGGCTGACATTCGTGA  
 GGATGACAACATTGCAATCATTGATGTGCCTGTCCCAGTTTCTCTGATAGTGACCCTGCAG  
 CAATTATTCATGACTTTGAAAAGGGAATGACTGCTTACCTGGACTTGTGTGCTGGGGAACCTGC  
 TATCTGATGCCCCCAATACTTCTATTGTTATGCCTCCAAAAATCTGGTAGAGCTCTTTGG  
 CAAACTGGCGAGTGGCAGATATCTGCCTCAAACCTTATGTGGTTCGAGAAGACCTAGTTGCTG  
 TGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGA  
 AAGTCCTTCGCCCTTCGTGCGAGAGACCTCTTGCTGGGTTTCAACAAACGTGCCATTGATAA  
 ATGCTGGAAGATTAGACACTTCCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAG**T**  
**AA**GAGGCAACAGATAGAGTGTCTTGGTAATAAGAAGTCAGAGATTTACAATATGACTTTAA  
 CATTAAGGTTTATGGGATACTCAAGATATTTACTCATGCATTTACTCTATTGCTTATGCTTT  
 AAAAAAAGGAAAAAAAAAAAACTACTAACCCTGCAAGCTCTTGTCAAATTTTAGTTTAAT  
 TGGCATTGCTTGTTTTTTGAAACTGAAATTACATGAGTTTCATTTTTTCTTTGCATTTATAG  
 GGTTTAGATTTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATTCATCC  
 GTTGTTTTTTTTGTTTGTGTTTTTTCTTTCCTTTAAGTAAGCTCTTTATTCATCTTATG  
 GTGGAGCAATTTTAAATTTGAAATATTTAAATTTGTTTTGAACTTTTTGTGTAAAAATATA  
 TCAGATCTCAACATTGTTGGTTTCTTTGTTTTTCATTTTGTACAACCTTCTTGAATTTAGA  
 AATTACATCTTTGAGTTCGTGTTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAATT  
 TTCATGAGACAGTCATTTTTAACTAATGCAGTGATTCTTTCTCACTACTATCTGTATTGTGG  
 AATGCACAAAATGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTGTATGAATTCTACAA  
 CCTATAATAAATTTTACTCTATACAAAAA

**FIGURE 26**

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
<subunit 1 of 1, 263 aa, 1 stop
<MW: 29741, pI: 5.74, NX(S/T): 1
MVKIAFNTPTAVQKEEARQDVEALLSRTVVRTQILTGKELRVATQEKEGSSGRCMLTLLGLSF
ILAGLIVGGACIYKYFMPKSTIYRGEMCFDSEDPA NSLRGGE PNFLPVTEEADIREDDNIA
IIDVPVPSFSDSDPAAIIHDFEKGMTAYLDLLLGNCYLMPLNTSIVMPK NLVELFGKLASG
RYLPQTYVVREDLVAVEEIRDVSNLGIFIYQLCNNRKSFR LRRRDLLLGFNKRAIDKCWKIR
HFPNEFIVETKICQE

```

**Type II transmembrane domain:**

amino acids 53-75

**N-glycosylation site.**

amino acids 166-170

**Casein kinase II phosphorylation site.**

amino acids 35-39, 132-136, 134-138

**N-myristoylation site.**

amino acids 66-72, 103-109

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 63-74

**FIGURE 27**

GGAGGAGGGAGGGCGGGCAGGCGCCAGCCCAGAGCAGCCCCGGGCACACGAGCTCTCT  
 CTTCCAGCCCAGGTGCCCCCACTCTCGCTCCATTGGCGGGAGCACCCAGTCTGTACGCC  
 AAGGAACTGGTCTGGGGGACCA**ATG**GTTTCGGCGGCAGCCCCAGCCTCCTCATCCTTCTG  
 TTGCTGCTGCTGGGGTCTGTGCCTGTACCGACGCCCGCTCTGTGCCCTGAAGGCCACGTT  
 CCTGGAGGATGTGGCGGGTAGTGGGAGGCCGAGGGCTCGTCGGCTCCTCCCCGAGCCTCC  
 CGCCACCCTGGACCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCACAACCTGGGG  
 GGCCCATCACCCCCACCAACTTCTGGATGGGATAGTGGACTTCTTCCGCCAGTACGTGAT  
 GCTGATTGCTGTGGTGGGCTCCCTGGCCTTTCTGCTGATGTTATCGTCTGTGCCGCGTCA  
 TCACCCGGCAGAAGCAGAAGGCCCTCGGCCTATTACCCATCGTCTTCCCAAGAAGAAGTAC  
 GTGGACCAAGTAGTACCGGGCCGGGGGCCCCCCGGGCCTTCAGTGAGGTCCCCGACAGAGCCCC  
 CGACAGCAGGCCCCGAGGAAGCCCTGGATTCTCCCGGCAGCTCCAGGCCGACATCTTGGCCG  
 CCACCCAGAACCTCAAGTCCCCACCAGGGCTGCACTGGGCGGTGGGGACGGAGCCAGGATG  
 GTGGAGGGCAGGGGGCAGAGGAAGAGGAGAAGGGCAGCCAGGAGGGGGACAGGAAGTCCA  
 GGGACATGGGGTCCCAGTGGAGACACCAGAGGCGCAGGAGGAGCCGTGCTCAGGGGTCTTG  
 AGGGGGCTGTGGTGGCCGGTGAGGGCCAAGGGGAGCTGGAAGGGTCTCTCTTGTTAGCCCCAG  
 GAAGCCCAGGGACCACTGGGTCCCCCGAAAGCCCTGTGCTTGACAGAGTGTCCACCCAG  
 TGTC**TAA**CAGTCTCTCCGGGGTGCCAGCCCTGACTGTGCGGCCCCCAAGTGGTACCTCCCC  
 GTGTATGAAAAGCCCTCAGCCCTGACTGCTTCTGACACTCCCTCCTTGGCTCCTGTGG  
 TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGGTGCCCCGGA  
 GGAATCTTACCAAGTGCCATCATCCTTCACCTCAGCAGCCCCAAAGGGCTACATCTACAGC  
 ACAGTCTCCCTGACAAAGTGAGGGAGGGCACGTGTCCCTGTGACAGCCAGGATAAAACATCC  
 CCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCCGCCCAAACACTACTTTTTTAAACA  
 GCTACAGGTAATAATCTGCAGCACCCACTCTGGAATACTGTCTTAATTTTCCTGAAGG  
 TGGCCCCCTGTTTCTAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGGCATTTAAATCCTC  
 TCAAGCGCTCTCAAGCACCCCCGGCCTGGGGGTGAGTTTCTCATCCCGCTACTGCTGCTGG  
 GATCAGGTTGAATGAATGGAACCTCTTCTGTCTGGCTCCAAAGCAGCCTAGAAGCTGAGGG  
 GCTGTGTTTGAGGGGACCTCCACCTGGGGAAGTCCGAGGGGCTGGGGAAGGGTTTCTGACG  
 CCCAGCCTGGAGCAGGGGGGCCCTGGCCACCCCTGTTGCTCACACATTGTCTGGCAGCCTG  
 TGTCCACAATATTCGTAGTCTCGACAGGGAGCCTGGGCTCCGTCTGCTTTAGGGAGGCT  
 CTGGCAGGAGGTCTCTCCCCCATCCCTCCATCTGGGGCTCCCCAACCTCTGCACAGCTCT  
 CCAGTGCTGAGATAATAATGCACCAGCACATAAACCTTTATTCCGGCTGAAAAAAAAAAAA  
 AAAGA

100%  
 90%  
 80%  
 70%  
 60%  
 50%  
 40%  
 30%  
 20%  
 10%  
 0%

**FIGURE 28**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAAPSLILLILLLLGSPATDARSVPLKATFLEDVAGSGEAEAGSSASSPSLPPPWTPAL
SPTSMGPQPPTTLGGPSPPTNFLDGIVDFFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA
SAYYPSSFPPKKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEEPCSGVLEGAVVAGE
GQGELEGSLLLAQEAQGPVGPPESPCACSSVHPSV
```

**Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 94-118

**N-myristoylation site.**

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,  
211-217, 238-244, 242-248

[illegible]

**FIGURE 30**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
MKFQGPLACLLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
AGSKVSEALQGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
ADAVRSGWQGVPGHSGAWETSGGHGIFGSQGGGLGGQGQNPFGGLGTPWVHGYPGNSAGSFGM
NPQGAPWQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGS
GSQSGSSSGSGSNGDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSGSRGDSGSESSW
GSSTGSSSGNHGSGSGGNGHKPGCEKPGNEARGSGESGIQGFRRGQGVSSNMREISKEGNRL
GGSGDNYRQGSSSWGSGGGDAVGVTNSETSPGMFNFDTFWKNFKSKLGFINWDAINKDQ
RSSRIP
```

**Signal peptide:**

amino acids 1-21

**N-glycosylation site.**

amino acids 265-269

**Glycosaminoglycan attachment site.**

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

**Casein kinase II phosphorylation site.**

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

**N-myristoylation site.**

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,  
 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,  
 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,  
 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,  
 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,  
 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,  
 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,  
 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,  
 383-389, 387-393, 389-395, 395-401

**Cell attachment sequence.**

amino acids 301-304

**FIGURE 31**

GACCGGTCCTCCGGTCTGGATGTGCGACTCTGCTGCAGCGAGGGCTGCAGGCCGCCGGGGCGGTGCTCACCG  
 TGCCTTGGCTGGTGGAGTTTCTCTCCTTTGCTGACCATGTTGTTCCCTTGTCTGGAAATTACCGGGACATCTTCA  
 CTCTCTGCTGCGGCTGTCACCGGAGCTTGGTGTGTGCGAGGAGTGAAGGGAAAGATTGTTTCTGTAACAAAGC  
 TGTCTGTACTTGTCTGCTGGGCTGGCTTTTCCAGATTCCCAAGTCCCTGAGGACTTGTCTTTCTGGAAGAGG  
 GTCCCTCATATGCGTTTGGGTGGACACAGTAGCCCCAGAGCATGGCTTGACAAATGCGCCTGTGGTGAGCAGC  
 AGCTGTCTTACACCTGCTGCCCTTACATCGGAGAGCTCCGGAAATCTGCTCGCTTCGTGGGTGTGAGGAGTAGTG  
 GACGGAGTGGGGCTTCTAGAGGAAATCACCCACCACACTACCCAGCTGGGAGCCAGCCTTCCAGACCA  
 GACGGGGCTGCAGGCAGCTTCGCCCAGGCCCTTTTCCACAAACAGCCGCCCTCTTCGCGCGGACCTTAGAGT  
 TCGTGCAAGAAATTTGATCAAACTGTGTCAACATATCAAGGCTACACTGGTGCGAGATCTGGTGCGCGAGG  
 CAGAGTCACTTCTCAAGAGCAGCTGGTGACACAGGAGAGGAGGGGGAGACCAGCCAGCTGTTGGAGATCT  
 TGTCTTCCAGCTGTGCCCTCACGGGGCCAGGCATTGGCCCTGGGGCGGGAGTCTGTCAAAGGAAGAGCCCTG  
 GGGCTGTGCGGGCGCTGCTCCAGAGGAGACCCCGGACGCCCTTCTGACGAGTGCAGAAACATTGCTGTGGGG  
 GTGCAACAGGAAGAGCTGCTTGTGCTGTGACCCAACTACAGCACTGATCAGGAGGAGGTGAAGACGACGAG  
 TGAATCGCACACTTCGAGCCCTAGGCTGCTGAACCTGCTGCCCGGGGGAGCGGAGGGGCTGCTCCCGGCCCTTGA  
 GTGCTCTCTTGGCCGTGGGGCCAGGGACCTTGACGAGGGAGTCTCCCGAGAGCATCTGGAACAGCTCTTAGGC  
 CAGCTGGGGCCAGAGCTGCGGTGCGCCAGTTCCTGTGCCACCTGCTGAGCAGCATCTGCGCAAAGTCTCTGTG  
 GAGTTAGTTCCTCTCTGTCGAGATCAAAATCTCTATCTAGGGCCCCCGGACAGTACAGCTGGAGAGAGG  
 CAGGCTGAGGCTTCTGCACATGCTGCTTTCTTGTGGAAGGAAGACTTTCGAGGCCCGGTTCGCTCGACGCTG  
 CTGCTGAGCCCCAAGAAATGTGGGGCTTCTGGCAGACCAAGGCCAAGGAGTGGGACTTGTCTGCTATTCTGCTA  
 CGGGAGCTGGTGGAAGAGGCTGATGGGACGGATGAGAGATAGAGGCTGCTGGGCCAGAGCTAGGGCTGCAGAGTGGCC  
 TGCCCAGGGGACTTGTCTGAAGAATTAGCAACACTGTCTAATCTGTTCTAGCGAGGCCACCTGCCAGAACCC  
 CAGCTAAGAGCCTGTGATTGCTGAGCCAAACCGGGGACTGTCTGGCCAGAGCTAGGGCTGGAAGTGGCC  
 CTGCTTGGGCATTGCACAGAACCTGGACCCCGCTCACGAGGAGGCCAAGTGCCTAATGCAGACCCCTCAC  
 TGGTTGGGGTGTAGCTGGGTCTACAGTCAGACTTCTGCTCTAAGGGTGTCACTGCTTGGCATCCCAACAGCCGA  
 ATCCTAGAGGAAGAGAGTGGCTGATTGGGATATGGCAGAAAGTCCAGAGATGCCAGTCTTGGAGTAGAA  
 GAGGTGGTGTGTTTATCTCTTGGATACTAAATGAAATGAGGTGTGTGGGCTGTCAACACAGATTAAGGCT  
 CATTTGCTATCCAGCATCTCTTAAACTTTGTAGTCTTGAATTCATGACAGAGGCAAAATGACTCTGCTCTAAC  
 TTATGAAGAAAGTTAAACATGAATCTTGGGAGTCTACATTTCTTATCACAGGAGCTGGAATGCCATCTCCTT  
 ATAAATGCCTAACACAGGCCGGGTCTGGTGGCTCATGCTGTATATCCAGCACTTTGAGAGGCTGAGGTGCGCG  
 GACTGCCTGAGGTGAGGAATTCAAGACCAGCTTGGCCAACTGGCAAAACCCCATCTCTACTAAAAATAAAAAA  
 TTATTAGCTGGGCATGGTGGTGTGTGCCGTGAATCCAGCTACTCAGGAGGATGAGGACAGGAGACTGCTTGAAC  
 CTGGAGTGGAGGTTGCAGTGAGCCGAGGTGCGACCACTGCACTCCAGTCTGGGTAAACAGAGCGAGACTTTAG  
 AAAAGCCTAACAAACAGATAAGGTAGGACTCAACCAACTGAAACCTGACTTCCCCCTGTACCTTACAGCCCTG  
 TGCAGGTAGTAACCTCTTGAGACTCTCCCTGACCAGGGACCAAGCAGAGGCAATTAGAGCTTTTATGAATAAA  
 CTGGTTTTTTTTAAAAAAGGGGCTTTATTAATAATCTCCCAACAGATGGCTCTGCAATCTGCGCAAGCTC  
 TTTTTTTTTTTTTTTTTAAAAAGGGCTTTATTAATAATCTCCCAACAGATGGCTCTGCAATCTGCGCAAGCTC  
 TGGGGCGTGTCTCTGAGGGAAGGCCGTGTTTTCCCTGAGGCGGGGCTGGGCTGTCCATGGGTCCGCGAGCTG  
 CGCGTGTGTGGCGGCTGGCGCTGTCTAGCTGCTTCTGCGGGGACAGAGCTGGCGGGTGTGGGGACACCGG  
 AGCTAAGACGAGGCTCTGGTGAGGGGTGAGGCTGTCTCTTAACCGACACCTCGAGGTGCTCTGAGATGCTG  
 GCTCCACCTTGAGTGGACCGGGGACGAGCTTGGCCGGTGTCTCTCTCTGAGGCTGAGTTCCTTCCCTGCTGA  
 GGGCCCTCTTGTGCAAGACCGAGATGGGTGGGTGTGGGGGACTCTGGGGAATGGCTGAGGAGCTACGTGT  
 GAAGAGGCGCGGTGTTGTTGGCTGACGCGCTGGAGCGCTCTCTCTGAGGCTGAGTTCCTTCCCTGCTA  
 ATGAAGAACATGCCCTCTCGGTGTCTCAGGCTTATAGGACTTGCCTCAGGAGTGCCCTTGGACGAGGCTAT  
 GTTATTTCACACTGTCTGTGCGAGTGTGGCTGGCACGTCTGGAATGGCCATGCTCCCTCTGCTGTGGTGGAC  
 CTGCGGTGCGGAGTGGCGACGAGGCGGGGCCAGAGCTGCGCTGGGGTGGGGAGGCGCCCGGAGG  
 CCTCAGAGAAATTTGGCTCCCGACACACAGGACGGGCGGCTCCCGCGCGCGCGCCACCCCTCAGG  
 GCGCGTGAAGAGTGGAGTTCGCGCTTGGGCTGCTGCGCAGCGAGTGCCTTGTGATGAGTGGCGACGCGG  
 TCGTCCGACAGCTGGAGACAGCGCCCTCCACAGCAGCAAGCGGCTGGCGCT

**FIGURE 32**

MCFLNKL LLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVDQQLLYTC  
 CPYIGELRKLLASWVSGSSGRSGGFMRKITPTTTTSLGAQPSQTSQGLQAQLAQAFFHNQPP  
 SLRRTVEFVAERIGSNVCVKHIKATLVADLVRQAESLLQEQLVTQGEEGGDP AQLLEILCSQL  
 CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENI AVGLATEKACAWLSANITAL  
 IRREVKA AVSRTLRAQGPEPAARGERRGCSRA

**Signal peptide:**

amino acids 1-18

**N-glycosylation site.**

amino acids 244-248

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 89-93

**Casein kinase II phosphorylation site.**

amino acids 21-25, 167-171, 223-227

**N-myristoylation site.**

amino acids 100-106, 172-178, 207-213

**Microbodies C-terminal targeting signal.**

amino acids 278-282



**FIGURE 33**

TCCCTTGACAGGCTCTGGTGGCTGGTTCGGGGTCTACTGAAGGCTGTCTTGATCAGGAACTG  
 AAGACTCTCTGCTTTTGCCACAGCAGTTTCTCGACGCTTCCCTGAGGTGTGAACCCACATCCC  
 TGCCCCAGGGCCACCTGCAGGACGCCGACACCTACCCCTCAGCAGACGCCGGAGAGAA**ATG**  
 AGTAGCAACAAAGAGCAGCGGTGAGCAGTGTTCGTGATCCTCTTTGCCCTCATCACCATCCT  
 CATCCTCTACAGCTCCAACAGTGCCAATGAGGTCTTCCATTACGGCTCCCTGCGGGGCCGTA  
 GCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGC  
 AACAAAGACTGCCCTCTCGGTGCCACCAGTGTGTGATTGTGACGAGCTCCAGCCACCTGCT  
 GGGCACCAGCTGGGGCCCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGCAC  
 CCACCACTGGCTACTCAGCTGATGTGGGCAACAAGACCACCTACCGCGTCGTGGCCCCATTCC  
 AGTGTGTTCCGCGTGCTGAGGAGGCCCCAGGAGTTTGTCAACCGGACCCCTGAAACCGTGTT  
 CATCTTCTGGGGGCCCCCGAGCAAGATGCAGAAGCCCCAGGGCAGCCCTCGTGCCTGTGATCC  
 AGCGAGCGGGCCTGGTGTTCCTCCCAACATGGAAGCATATGCCGCTCTCTCCCGGCCGATGCGG  
 CAATTTGACGACCTCTTCCGGGTGAGACGGGCAAGGACAGGGAGAAGTCTCATTCTGTGGTT  
 GAGCACAGGCTGGTTTACCATGGTGATCGCGGTGGAGTTGTGTGACCAGTGCATGTCTATG  
 GCATGGTCCCCCCTACTACTGCAGCCAGCGGCCCGCCCTCCAGCGCATGCCCTACCACTAC  
 TACGAGCCCAAGGGGCCGACGAATGTGTACCTACATCCAGAATGAGCACAGTCGCAAGGG  
 CAACCACCACCGCTTCATCACCGAGAAAAGGGTCTTCTCATCGTGGGCCAGCTGTATGGCA  
 TCACCTTCTCCACCCCTCCTGGACCT**TAG**GCCACCCAGCCTGTGGGACCTCAGGAGGGTCAG  
 AGGAGAAGCAGCCTCCGCCAGCCGCTAGGCCAGGGACCATTCTCTGGCCAATCAAGGCTTG  
 CTGGAGTGTCTCCCAAGCCAATCAGGGCCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCC  
 TGGGGAATCTGTTGGCGAATCAGGGATTGGGAGTCTATGTGGTTAATCAGGGGTGTCTTTC  
 TTGTGCAGTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGTATTTCTGAGTCAATCTG  
 AGGCTAAGGACATGTCTTTCCCATGAGGCCTTGGTTCAGAGCCCCAGGAATGGACCCCCA  
 ATCACTCCCCACTCTGCTGGGATAATGGGGTCCCTGCCAAGGAGCTGGGAACCTTGGTGTG  
 CCCCCCAATTTCCAGCACAGAAAGAGAGATTGTGTGGGGGTAGAAGCTGTCTGGAGGCC  
 GGCCAGAGAATTTGTGGGGTGTGGAGGTTGTGGGGCGGTGGGAGGTTCCAGAGGTGGGA  
 GGCTGGCATCCAGGTCTTGGCTCTGCCCTGAGACCTTGGACAAACCCCTCCCCCTCTCTGGG  
 CACCCTCTGCCCCACACAGTTTCCAGTGCGGAGTCTGAGACCTTTCCACCTCCCCACAA  
 GTGCCCTCGGGTCTGTCTTCCCGTCTGGACCTCCAGCCATATCCCTTGTCTGGAAGGCT  
 CAGCTCTTTGGGGGTCTGGGGTGACCTCCCCACCTCCTGGAAAACCTTTAGGGTATTTTTC  
 GCAAACTCCTTCAGGGTTGGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTTCT  
 TAGCCCCCTCAGCCAGCTGCCATTAGCTTGGCTCTTAAAGGGCCAGGCCTCCTTTCTGCCCT  
 CTAGCAGGGAGGTTTTCCAACTGTGTGGAGGCGCCTTTGGGGCTGCCCTTGTCTGGAGTCA  
 CTGGGGGCTTCCGAGGGTCTCCCTCGACCTCTGTCTGCTTGGGATGGCTGTGGGAGTGT  
 ATCACCTGGGTCTGTGCCCTGGCTGTATCAGGCACTTTATTAAGCTGGGCCTCAGTGG  
 GGTGTGTTTGTCTCTGCTCTTCTGGAGCCTGGAAAGGAAAGGCTTCAGGAGGAGGCTGTGA  
 GGCTGGAGGGACAGATGAGGAGGGCCAGCAGCTAGCCATTGCACATGGGGTGATGGGTGG  
 GGGCGGTGACTGCCCCAGACTTGGTTTTGTAAATGATTTGTACAGGAATAAACACACCTACGC  
 TCCGGA

**FIGURE 34**

MSSNKEQRSADVILFALITILILYSSNSANEVFHYGSLRGRSRRPVNLKKWSITDGYVPIL  
 GNKTLPSRCHQCIVIVSSSSHLGTLGPEIERAECTIRMNDAPTGTGYSADVGNKTTYRVVAH  
 SSVFRVLRRPQEFVNRTPTVFIFWGPSPKMQKPPQGSLVRVIQRAGLVFPNMEAYAVSPGRM  
 RQFDDLFRGETGKDREKSHSWLSTGWFTMVIARELCHVHVYGMVPPNYCSQRPRLRMPYH  
 YYEPKGPDECVTYIQNEHSRKGNNHRRFITEKRVFSSWAQLYGITFSHPST

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 9-31 (type II)

**N-glycosylation site.**

amino acids 64-68, 115-119

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 50-54

**Casein kinase II phosphorylation site.**

amino acids 3-7, 29-33, 53-57, 197-201

**Tyrosine kinase phosphorylation site.**

amino acids 253-262

**N-myristoylation site.**

amino acids 37-43, 114-120, 290-294

**FIGURE 35**

**FIGURE 36**

MLRGTMTAWRGMRPEVTLACLLLATAGCFADLNEVPQVTVQASTVQKPGGTIVLGCVVVEPP  
 RMNVTWRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL  
 ANLQDFKLDVQHVIEVDEGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMP SGNLQ  
 IVNASQDEDEGMYKCAAYNPVTQEVKTS GSSDRLRVRRSTAEAAARI IYPPEAQTIIIVTKGQSL  
 ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGA  
 AVILYNVQVFEPPEVTMELSQLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLS  
 RRALRVLSMGPEDEGVYQCAENEVGSAAHAVVQLRTSRPSITPRLWQDAELATGTPPVSPSK  
 LGNPEQMLRGQPALPRPPTSVGPASPKCPGEKGQGAPAEAPIILSSPRTSKTDSYELVWRPR  
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGE  
 GQTAMVTFRTGRRPKPEIMASKEQQIQRDDPGAS PQSSSQPDHGR LSPPEAPDRPTISTASE  
 TSVYVTWIPRGNNGGFFIQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGT SYKFRV  
 RALNMLGESEPSAPSRPYVVS GYSGRVYERPVAGPYITFTDAVNETTIMLKWMIYPASNNNT  
 PIHGFYIYYRPTDSNDSDYKKDMVEGDKYWHSISHLQPETS YDIKMQCFNEGGESEFSNVM  
 ICETKARKSSGQFGRLPPTLAPPQPLPETIERPVGTGAMVARSSDLPYLIVGVVLGSIVL  
 IIVTFIPFCLWRAWKQKHTTDLGFPRSALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRA  
 CANGIHMNRGCP SAAVGYPGMKPQQHCPGELQQQSDTSSLLRQTHLGNGYDPQSHQITRGPK  
 SSPDEGSFLYTL PDDSTHQLLQPHHDCQQRQEQPAAGVQSGVRRAPDSPVLEAVWDPPFHSG  
 PPCCGLGLVPVEEVDSPDSCVSGGDWCQHPVGAYVVGQEPGMQLSPGPLVRVSFETPPLTI

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 16-30 (type II), 854-879

**FIGURE 37**

CGGGAGGCTGGGTCGTCATGATCCGGACCCCATTTGTCGGCCTCTGCCCATCGCCTGCTCCTC  
 CCAGGCTCCCGCGGCCGACCCCGCGCAAC**ATG**CAGCCACGGGCCGCGAGGGTTCCCGCGC  
 GCTCAGCCGGCGGTATCTGCGGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGC  
 CCGTAACCCGCGCGGAGACCAGCCGGGCGCCCCAGAGCCCTCTCCACGCTGGGCTCCCC  
 AGCCTCTTACCACGCGGGTGTCCCCAGCGCCCTCACTACCCAGGCCTCACTACGCCAGG  
 CACCCCCAAAACCTGGACCTTCGGGGTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCG  
 TGGACGGCCACAATGACCTGCCCCAGGTCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT  
 GTTAACCTGCGAAATTTAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT  
 GGGTGCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCAGACCAGACTGCCGTGCGCC  
 TCGCCTGGAGCAGATGACCTCATTACCGCATGTGTGCCTCCTACTCTGAACCTCGAGCTT  
 GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAAGCTGGCCTGCCTCATTTGGCGTGNAGGG  
 TGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCT  
 ACCTGACACTTACCTTACCTGCAGTACACCATGGGCAGAGAGTTCCACCAAGTTCAGACAC  
 CACATGTACCCAACGTACGCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAA  
 CCGCCTGGGCATGATGATAGATTTGTCTATGCATCGGACACCTTGATAAGAAGGGTCTTG  
 AAGTGTCTCAGGCTCCTGTGATCTTCTCCACTCAGCTGCCAGAGCTGTGTGTGACAATTG  
 TTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGACACT  
 GTCCATGGGGGTGCTGCAAGTGAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG  
 ACCACATCAGGGCAGTCATTGGATCTGAGTTCATCGGGATTGGTGGAATTTATGACGGGACT  
 GGCCGGTTCCCTCAGGGGCTGGAGGATGTGTCCACATACCAGTCTGATAGAGGAGTTGCT  
 GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCTTTCGTGGAACCTGCTGCGGGTCT  
 TCAGACAAGTGGAAGAGTGAGAGAGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTTT  
 CCATATGGGCACTGAGCAGATCTGCCACTCCACCTCGTGCCCTCAGAATGGACACCAGGC  
 TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCTGGAGGTCTCAAATGCCT  
 CCCCATACCTTGTTCCAGGCCTTGTGGCTGCTGCCACCATCCCAACCTTCACCAGTGGCTC  
 TGC**TGA**CACAGTCGGTCCCGCAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCCT  
 AGTTCATTCAACGATATGCTGAGAATAAACATGTTACACATGGAATA

**FIGURE 38**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRYLRRLLLLLLLLLLLLLRQPVTTRAETTPGAPRALSTLGSPSLFTTPGVFS
ALTTPGLTTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQ
TSLDRLRDGLVGAQFWSASVSCSQSDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS
QKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTCTPWAESSSTKFRHHMYTNVSGLT
SFGEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNLLNVDPDDILQL
LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDV
STYPVLIEELLSRXWSEELQGVLRGNLLRVFRQVEKVREESRAQSPVEAEFFYQGLSTSCH
SHLVPQNGHQATHLEVTKQPTNRVPWRSSNASPYLVPGLVAAATIPFTQWLC
```

**Important features of the protein:****Signal peptide:**

amino acids 1-36

**Transmembrane domain:**

amino acids 313-331

**N-glycosylation sites.**

amino acids 119-122, 184-187, 243-246 and 333-336

**N-myristoylation sites.**

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 136-146

**FIGURE 39**

TGCTAGGCTCTGTCCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA  
 TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCCAGCAAGCCTGATAAGC**ATG**  
 AAGCTCTTATCTTTGGTGGCTGTGGTCCGGGTGTTTGTGGTGCCCCAGCTGAAGCCAACAA  
 GAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA  
 TTTACAACCAGAAATGTATCCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCA  
 GTGCCCTGGCCATGACGTGGAGGCCTACTGCCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG  
 CACCACCACCATCAAGGTCATCATTGTATCTACCTGTCCGTGGTGGGTGCCCTGTGTGCTCT  
 ACATGGCCTTCTCTGATGCTGGTGGACCCCTCTGATCCGAAAGCCGGATGCATACACTGAGCAA  
 CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG  
 GGGACCCCAGCAAAACACAGTCTTGAGCGGTGTGGAAGGTGCCAGCAGCGGTGGAAGCTGC  
 AGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGC**TAGAT**GGGCTGG  
 TGTGGTTGGGTCAAGGCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGGG  
 CTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAAGCCTGTGGCATTTTTCCCTCCTT  
 CTCCCTAACTTTAGAAATGTTGTACTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCT  
 GATCTCTGTTGTCTTCTTGGGTCTTTGGGTTGAAGGGAGGGGAAGGCAGGCCAGAAGGGA  
 ATGGAGACATTGAGGCGGCCTCAGGAGTGGATGCGATCTGTCTCTCCTGGCTCCACTCTTG  
 CCGCCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCCCTTGAAGATAAAGCTGGGTCTTCA  
 GGAACCTCAGTGTCTGGGAGGAAAGCATGGCCAGCATTACAGCATGTGTTCTTCTGCAGTG  
 GTTCTTATCACCACCTCCCTCCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG  
 AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCACTGGGTCTTCAGGGTGCACTGGA  
 AGCTGGTGTTCGCTGTCCCTGTGCACTTCTCGCACTGGGGCATGGAGTCCCATGCATACT  
 CTGCTGCCGGTCCCCCTCACCTGCACTTGAGGGGTCTGGGCAGTCCCTCCTCTCCCCAGTGT  
 CACAGTCACTGAGCCAGACGGTCCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA  
 CACCACAGCCCCGTGACTTGGGTTGCCTCTTGTCCTGAACTTCGTTGTACCACTGCATGGA  
 GAGAAAATTTTGCTCTTGTCTTAGAGTTGTGTGTAATCAAGGAAGCCATCATTAAATTG  
 TTTTATTTCTCTCA

**FIGURE 40**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278

<subunit 1 of 1, 183 aa, 1 stop

<MW: 20574, pI: 6.60, NX(S/T): 3

MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPM  
PVPGHDEVEAYCLLCECRYEERSTTTIKVIVIVYLSVVGALLLYMAFLMLVDPLIRKPDAYTE  
QLHNEEENEDARSMAAAAASLGGFRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS

**Important features:****Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 90-112

**N-glycosylation sites.**

amino acids 21-24, 38-41 and 47-50



**FIGURE 41**

AGCGGGTCTCGCTTGGGTTCGCTAATTTCTGCTCTGAGGCGTGAGACTGAGTTCATAGGTCCTGGGTCCCCGA  
 ACCAGGAAGGGTTGAGGGAACACAACTGCAAGCCCCCGGACCCCAAGTGAGGGGCCCCGTGTGGGGTCTCC  
 TCCCTTTGCTATCCCAACCCCTCGGGCTTTGCGTCTTCTCGGGACCCCTCGCGGGAGATGGCGCGGTGTATG  
 CGGAGCAAGGATTCTGCTCTGCTGCTGCTCTACTGGCCGCGGTGCTGATGGTGGAGAGCTCACAGATCGGCAGT  
 TCGCGGGCCAAATCAACTCCATCAAGTCTCTCTGGCGGGGAGACGCTGTGAGGCGCCCAATCGATCTGCG  
 GGCATGTACCAAGGACTGGCATTCGGCGGCAGTAAGAAGGGGCAAAACCTGGGCGAGCCCTACCTTTGTAGCAGT  
 GATAAGGAGTGTGAAGTTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATCGGCCTGCATGGTGTGCGGAGA  
 AAAAAGAGCGCTGCCACCGAGATGGCATGTGCTGCCCGAGTACCCGCTGCAATATGGGATCTGTATCCCGAGTT  
 ACTGAAAGCATTTAAACCCCTCACATCCCGCTCTGGATGGTACTCGGCACAGAGATCGAAACCCACGGTCATTAC  
 TCAAAACATGACTTGGGATGGCAGAACTAGGAAGACACACACTAAGATGTGCATATAAAAGGGCATGAAGGA  
 GACCCCTGCTACGATCATCAGACTGCATTGAAGGTTTTGCTGTGCTCGTCATTCTGACCAAAATCTGCAAA  
 CCAATGCTCCATCAGGGGAAGTCTGTACAAACCAAGCAAGAGGGTTCTCATGGGCTGGAAATTTTCCAGCGT  
 TGCAGCTGTGCAAGGGCTGTCTTGCAAAGTATGGAAGATGCCACCTACTCCTCCAAAGCCAGACTCCATGTG  
 TGTGAGAAATTTGATACCACTTGAAGAACATCATCAATTGCAGACTGTGAAGTTGTGTATTTAATGCATTATAG  
 CATGCTGGAATAAGGTTTCAGATGCAGAGAAATGGCTAAAATAAGAAACGTGATAAGAATATAGATGATCACAA  
 AAGGGGAGAAAGAAACATGACATGAATAGATAGAAATGGGTGCAAAATGCAGTGCAGCCAGTGTTCATTATG  
 CAACTTGTCTATGTAATAATGTACACATTTCTGGAAATGCTATTATTAAGAGAACCAAGCACAGCTGGAATTT  
 ACTGATGAGTAGCATGTGACTTTCCARGAGTTAGGTTGTGCTGGAGGAGAGGTTTCTTCAGATTGCTGATTGC  
 TTATACAAATAACCTACATGCCAGATTTCTATTCAACGTTAGAGTTTAAACAAATACTCCTAGAATAACTTGTTA  
 TACAATAGGTTCTAAATAATAAAATTTGCTAAACAGAAATGAAACATGGAGCATTTGTTAATTTACAAACAGAAAT  
 TACCTTTTGATTGTAACTACTTCTGCTGTTCAATCAGAGTCTTGGTAGATAAGAAATAAATCACTCAATAT  
 TTCCAAATAATTCACAAATAATGGCCAGTTGTTAGGAAGGCTTTAGGAAGCAATAAATAACAAACAAACAG  
 CCACAAATACTTTTITTTTCAAATTTTAGTTTTACCTGTAATTAATAAGACCTGATACAGACAAACACTTCC  
 TTCAGATTCTACGGAATGACATATATCTCTCTTTATCCCTATGTGATTCCGTCTGATGTTATATTTTCCA  
 AACTATACCCATAAAATTTGACTAGTAAAATACTTACACAGAGCAGAAATTTACAGATGGCCAAAAAATTTAAA  
 GATGTCCCAATATATGTGGGAAAAAGCTAACAGAGAGATCATTTATTTCTTAAAGATTTGCCCAATCTATATTT  
 GATAGAAATAGATTGGTAAATACATGTATTATACATACTCTGTGGTAATAGAGACTTAAGCTGGATCTGTACTG  
 CACTGGAGTAAGCAAGAAATTTGAGAAACCTTTTCGTTTGTTCAGGTTTGGCAACACATAGATCATATGTCTG  
 AGGCACAAGTTGGCTGTTCACTTTTGAACCCAGGGGATGCACAGCTTAAATGAATATCTGCATGGGATTTGCTAT  
 CATAATATTTACTATGCAGATGAATTCAGTGTGAGTCCGTGTGCGGCTACTATCCTCAAATATTTATTTTATAG  
 TGCTGAGATCTCAAATAATCTCAATTTCAGGAGGTTTCACAAAATGTACTCCTGAAGTAGACAGAGTAGTGAGG  
 TTTCAATGGCCCTATAAGCTCTGACTAGCCAAATGGCATCATCCAATTTTCTTCCCAAACTCTGCAGCATCTG  
 CTTTATTTGCCAAGGGCTAGTTTTCGTTTTCTGCAGCCATTGCGGTTAAAAAATATAAGTAGATAACTTTGTAAA  
 AACTGCATATTTGCTAATCTATAGACACCACAGTTTCTAAATTTCTTGAACCACTTTACTACTTTTTTTAAACT  
 AACTCAGTCTCAAATACTTTGTCTGGAGCACAAAACATAAAGGTTATCTTATAGTCGTGACTTTAAACTTTTG  
 TAGACCACAATTCATTTTATGTTTTCTTTACTTAATCCCATCTGCAGTCTCAAAATTTAAGTTCTCCAGTAG  
 AGATTGAGTTTGAGGCTGTATATCTATTTAAATTTCAACTTCCCACATATATTTACTAAGATGATTAAAGACTTA  
 CATTTTCTGCAGGCTGCAAAAACAAAATTTAAACTAGTCCATCCAGAACCAAGGTTGTATAAACAGGT  
 TGCTATAGCTTTGTGAATGAAATGGAACATTTCAATCAACATTTTCTATATAACAAATATTATATTACAAAT  
 TTGGTTTTCTGCAATATTTTCTTATGTCCACCTTTTAAAAATTTATTTTGAAGTAATTTTATTACAGGAATG  
 TTAATGAGATGTATTTCTTATAGAGATTTTCTTACAGAAAGCTTTGTAGCAGAAATATTTTGCAGCTATTGAC  
 TTGTAAATTTAGGAAAAATGTATAATAGATAAAATCTATTAATTTTCTCCTCTAAAAACTGAAAAAATAA  
 AAAAAAATAAATAAATAA

**FIGURE 42**

MAALMRSKDSSCCLLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA  
FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQSSACMVCRRKKRCHRDGMCCPSTRCNN  
GICIPVTESILTPHIPALDGTNRHNRHGHYSNHDLGWQNLGRPHTKMISHKGHEGDPCLRS  
SDCIEGFCCARHFWTKICKPVLHQGEVCTQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS  
SKARLHVCQKI

**Signal peptide:**

amino acids 1-25

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**FIGURE 43**

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAATCCACCTACCTTGGCCTCCCAA  
 GTGTTGGGATTACAGGCGTGAGCCACCGCGCCGCCAACATCACGTTTTTAAAAATTGATT  
 TCTTCAAATTCATGGCAAATATTTCCCTTCCCTTTAACTTCTTATGTCAGAATGAGGAAGGA  
 TAGCTGCATTTATTTAGTCAGTTTTTCATTGCATAGTAATATTTTCATGTAGTATTTCTAAG  
 TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTGAAAATACCTTG  
ATGTGTTTTAAAGCCTTGGGCAGAAATCTGTATTGTTGAGGATTTGTCTTTTATCCCCCT  
 TTTAAAGTCATCCGTCCTTGGCTCAGGATTTGGAGAGCTTGCACCACCAAAATGGCAAACA  
 TCACCAGCTCCAGATTTTGGACCAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC  
 CCAAGTACACAGCAGAATAGTACAAGTCACCTACAACACTACTTCTTGGGACCTCAAGCC  
 CCCAACATCCCAGTCCCTCAGTCCTCAGTCATCTTGACTTCAAATCTCAACCTGAGCCATCCC  
 CAGTTCCTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCACTGTTCTCTCT  
 CCTGGTTTGGAGTCCTTCTCTCCAGGCAAACTTCGAGAATCAACACCTGGAGACAGTCC  
 CTCCACTGTGAACAAGCTTTTGCAGCTTCCCAGCAGCACCATTGAAAATATCTCTGTGTCTG  
 TCCACCAGCCACAGCCCAACACATCAAACCTTGCTAAGCGGCGGATACCCAGCTTCTAAG  
 ATCCAGCTTCTGCAGTGGAATGCCTGGTTCAGCAGATGTCACAGGATTAATGTGCAGTT  
 TGGGGCTCTGGAATTTGGGTGAGAACCCTTCTCTCTCTGAATTTGGATCAGTCCAAGCAGTG  
 AAAATAGTAATCAGATTCCCATCAGCTTGATTCGAAGTCTTTAAGTGAGCCTTTGAATACA  
 TCTTTATCAATGACCAGTGCAGTACAGAATCCACATATACAACCTCCGTCATTACCTCCTG  
 CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTTCTCTTATGACC  
 AGAGTCTGTGCATAACAGGATCCCATACCAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCA  
 GGAACCATCATGAATGGACATGGTGGTGGTGAAGTCAGCAGACACTAGACAGTAAGTATAG  
 CAGCAAGCTACTCTTGTGCATGGCTGGTGGCAACCAACAGAGGAAGAGGATAGCTCACGTGA  
 TGTGGAACACACAGTTGGTCAATGGCTCATTGCTTAAAGCAGCCCTTTTGCTTTTTTGT  
 TTTTGACACAGGTGTTGGCTGTGGTGTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT  
 GGTGGTCTCATATTCTTCTGCCCTAATCAGACTGCACCACAAGTCGAGCATACAGTATGCAT  
 TTTAAAGATGCTTGGGCCAGGCGGGGTGGCTGATGCCCATAAATCCCAGTGCTTTGGGGGGCC  
 AAGGCAGGCAGATTGCCCAAGCTCAGGAGTTTGAGACCACCTGGGCAACATGGTGAAACTC  
 TGTCTCTACTAAATACGAAAACTAGCCGGGTGTGGTGGCGGCGCTGCCTGTAATCCCAG  
 CTACTTGGGAGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC  
 GTCTGAAAAGA

**FIGURE 44**

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT  
 PSTQQNSTSHPTTTTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAQVTVPP  
 PGLESFPSQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPPKHIKLAKRRIPPASK  
 IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSSENSNQIPISLYSKSLSEPLNT  
 SLSMTSAVQNSTYTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQSPVSSSESAP  
 GTIMNGHGGGRSQQTLDISKYSSKLLLSWLVP TKQRKRIAHVMWKT PVGQWLIR

**Signal peptide:**

amino acids 1-24



**FIGURE 45**

GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCCATGGCGCTGCCATCCCCGAATCCTGCT  
 TTGGAAACTTGTGCTTCTGCAGAGCTTGTGTTCTCCTGCACCTCAGCGGTGGAGGAGACGG  
 ACGCGGGGCTGTACACCTGCAACCTGCACCATCTACTTGCACCTCTACGAGAGCCTGGCC  
 GTCCGCTGGAGGTACCGACGGCCCCCGGCCACCCCGCCTACTGGGACGGCGAGAAGGA  
 GGTGCTGGCGTGGCGCGCGGCCACCCGCGCTTCTGACCTGCGTGAACCGGGGACGTGT  
 GGACCGACCGGCACGTGGAGGAGGCTAACAGGTGGTGCATGGGACCGGCAGCCGCCGGG  
 GTCCCGCACGACCGCGCGGACCGCCTGCTGGACCTCTACGCGTGGGCGAGCGCCGCGCCTA  
 CGGGCCCTTTTCTGCGCGACCGGTGGCTGTGGGCGCGGATGCCTTTGAGCGCGGTGACT  
 TCTCACTGCGTATCGAGCCGTGGAGGTGCGCGAGGGGACCTACTCTGCCACCTGCAC  
 CACCATTACTGTGGCCTGCACGAACGCCGCGTCTTCCACCTGACGGTGCAGCAACCCACGC  
 GGAGCCGCCCCCGGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGGCGCCCCAGGCCACG  
 ACCCCACACTGGCGCGCGGCCACAACGTATCAATGTATCATCGTCCCCGAGAGCCGAGCCAC  
 TTCTTCCAGCAGCTGGGCTACGTGCTGGCCACGCTGCTGCTCTTATCCTGCTACTGGTCAC  
 TGTCCTCCTGGCGCCCGCAGGCGCGCGGAGGCTACGAATACTCGGACCAAGTTCGGAA  
 AGTCAAAGGGGAAGGATGTTAACTTGGCGGAGTTCGCTGTGGCTGCAGGGGACAGATGCTT  
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAACAACATCCTGAAGGAGAGGGCGGAGCT  
 GGCCCCAGCCCCCTGCCCTGCCAAGTACATCGACCTAGACAAAGGGTTCGGGAAGGAGAACT  
 GCAAATAGGGGAGGCCCTGGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC  
 CTCGGGGCATCTCCTGATGCTCCGGGGCTCACCCCCCTTCCAGCGGCTGGTCCCGCTTTCCCT  
 GGAATTTGGCCTGGGCGTATGCAGAGGCCGCTCCACACCCCTCCCCAGGGGCTTGGTGGC  
 AGCATAGCCCCACCCCTGCGGCCTTTGCTCACGGGTGGCCCTGCCACCCCTGGCACAAAC  
 AAAATCCCCTGATGCCATCATGCCCTCAGACCCCTTCTGGGCTCTGCCCGCTGGGGGCTG  
 AAGACATTCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAACTGGGGTCAGCCTCA  
 GGGCAGGAGTCCCACTCCTCCAGGGCTCTGCTCGTCCGGGGCTGGGAGATGTTCTGGAGGA  
 GGACACTCCCATCAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGCAGGAGTCCCACT  
 CCTCCTGGGGTGTGCTGCCACCAAGAGCTCCCCACCTGTACCACCATGTGGGACTCCAG  
 GCACCATCTGTTCTCCCCAGGGACCTGCTGACTTGAATGCCAGCCCTTGCTCCTCTGTGTTG  
 CTTTGGGCCACCTGGGGCTGCACCCCTGCCCTTTCTCTGCCCCATCCCTACCCTAGCCTTG  
 CTCTCAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCTTGACACCCCTCCCTT  
 GGACTCTGCCTGGGCTGGAGTCTAGGGCTGGGGCTACATTGGCTTCTGTACTGGCTGAGGA  
 CAGGGGAGGAGTGAAGTTGGTTGGGGTGGCCTGTGTTGCCACTCTCAGCACCCACATT  
 GCATCTGTGGTGGACCTGCCACCATCACAATAAAGTCCCCATCTGATTTTTAAAAA  
 AAAAA

**FIGURE 46**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618
<subunit 1 of 1, 341 aa, 1 stop
<MW: 38070, pI: 6.88, NX(S/T): 1
MALPSRILLWKLVLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTD RHVEEAQQVVHWDRQPPGVPHDRADRLDL
YASGERRAYGPLFLRDRVAVGADAFERGFSLRIEPLLEVADEGTYSCHLHHHYCGLHERRVF
HLTVAEPHAEP PPRGSPNGSSHSAGPGDPTLARGHNVINVIVPESRAHFFQQLGYVLATL
LLFILLLVTVLLAARRRRGGYEYSDQKSGKSKGKDVNLAEFAVAAGDQMLYRSEDIQLDYKN
NILKERAELAHSPLPAKYIDLDKGFRKENCK
```

**Important features:****Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 237-262

**N-glycosylation site.**

amino acids 205-208

**Cell attachment sequence.**

amino acids 151-154

**Coproporphyrinogen III oxidase proteins.**

amino acids 115-140

**FIGURE 47**

CGCCGGAGGCAGCGCGCGCGTGGCGCAGCGCGCAC**ATG**GCCGTTGTCTCAGAGGACGACTTT  
 CAGCACAGTTCAAACTCCACCTACGGAACCAACAAGCAGCAGTCTCCGAGCTGACCAGGAGGC  
 ACTGCTTGAGAAGCTGCTGGACCGCCCGCCCCCTGGCCTGCAGAGGCCGAGGACCGCTTCT  
 GTGGCACATACATCATCTTCTTCCAGCCTGGGCATTGGCAGTCTACTGCCATGGAAGTCTCTTT  
 ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCCCAGCCACCGGGGA  
 GGACCCTGAGGGCTCAGACATCCTGAACTACTTTGAGAGCTACCTTGCCGTTGCCTCCACCG  
 TGCCCTCCATGCTGTGCCTGGTGGCCAACTTCTGCTTGTCAACAGGGTTGCAGTCCACATC  
 CGTGCTCTGGCCTCACTGACGGTCATCCTGGCCATCTTCATGGTGATAACTGCACTGGTGAA  
 GGTGGACACTTCTCTCGGACCCGTGGTTTTTTTTGCGGTCACCAATTGTCTGCATGGTGATCC  
 TCAGCGTGCCTCCACTGTCTTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTCTCTATG  
 AGGAACCTCCCAAGCACTGATATCAGGAGGAGCCATGGGCGGACGGTCAGCGCCGTGGCCTC  
 ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCTGACGG  
 CCACCATCTTCTCGTGCTCTGCATGGGACTCTACCTGCTGCTGTCCAGGCTGGAGTATGCC  
 AGGTACTACATGAGGCTGTCTTGGCGCCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCCA  
 GGACTCCCTCAGTGCCCTTCCGGTGGCTCCAGATTATTGATTCCACACACCCCTCTCC  
 GCCCCATCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTCACTACGCTCTTCTTCATCACC  
 AGCCTCATCTACCCCGCGTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCTCACT  
 GTGGACCAACAAGTTTTTCATCCCCCTCACTACCTTCTCTGTACAACCTTGTGACCTAT  
 GTGGCCGGCAGCTCACCGCTGGATCCAGGTGCCAGGGCCCAACAGCAAGGCGCTCCAGGG  
 TTCGTGCTCCTCCGGACCTGCCCTCATCCCCCTCTTCGTGCTCTGTAACCTACGAGCCCCGCT  
 CCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCCGCACTCCTCAGCTCCCTGCTGG  
 GGCTCAGCAACGGCTACCTCAGCACCCCTGGCCCTCCTCTACGGGCCCTAAGATTGTGCCAGG  
 GAGCTGGCTGAGGCCACGGGAGTGGTGATGTCCTTTTATGTGTCTTGGGCTTAACACTGGG  
 CTCAGCCTGCTCTACCTCCTGGTGCACTCATCT**TAGA**AGGGAGGACACAAGGACATTGGTG  
 CTTCAGAGCCTTTGAAGATGAGAAGAGAGTGCAAGAGGGCTGGGGCCATGGAGGAAAGGCC  
 TAAAGTTTCACTTGGGGACAGAGAGCAGAGCACACTCGGGCCTCATCCCTCCCAAGATGCCA  
 GTGAGCCACGTCATGCCATTCCGTGCAAGGCAGATATTCAGTTCATATTAAACAGAACT  
 CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTACAGCTGATGGTTA  
 ACATTCCACCTTCTTTCTAGCCCTTCAAAGATGCTGCCAGTGTTCGCCCTAGAGTTATTACA  
 AAGCCAGTGCCAAACCCAGCCATGGGCTCTTTGCAACCTCCAGCTGCGCTCATTCAGCT  
 GACAGCGAGATGCAAGCAATGCTCAGCTCTCCTTACCTTGAAGGGGTCTCCTTGGAAATGGA  
 AGTCCCCCTGGCATGGTCAGTCCTCAGGCCAAGACTCAAGTGTGCACAGACCCCTGTGTCT  
 CGGGTGAACAACTGCCCACTAACACAGACTGGAAAAACCCAGAAAGATGGGCCCTTCATGAAT  
 GCTTCATTCCAGAGGGACGAGGGCCTCCCTGTGCAAGGGATCAAGCATGTCCTGGCCTGGG  
 TTTTCAAAAAAGAGGATCCTCATGACCTGGTGGTCTATGGCTGGTCAAGATGAGGGTCTC  
 TTTCACTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGC  
 GTATTCAAAAA

**FIGURE 48**

MAVVSDDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGGLQRPEDRFCGTYYIFFSLGI  
 GSLLPWNFFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL  
 LVNRVAVHIRVLASLTVILAI FMVITALVKVDTSWTRGFFAVTIVCMVILSGASTVFSSSI  
 YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVNSALAFFLTATIFLVLCMGly  
 LLLSRLEYARYYMRPVLAHVFSGEEELPQDSL SAPSVASRFIDSHTPPLRPILKKTASLGF  
 CVTYVFFITSLIYPVCTNIESLNKSGSLWTKFFIPLTTFLLYNFADLCGRQLTAWIQVP  
 GPNSKALPGFVLLRTCLIPFLVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLAL  
 LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

**Transmembrane domain:**

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,  
 305-330, 448-472

1-10  
11-20  
21-30  
31-40  
41-50  
51-60  
61-70  
71-80  
81-90  
91-100  
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111-120  
121-130  
131-140  
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731-740  
741-750  
751-760  
761-770  
771-780  
781-790  
791-800  
801-810  
811-820  
821-830  
831-840  
841-850  
851-860  
861-870  
871-880  
881-890  
891-900  
901-910  
911-920  
921-930  
931-940  
941-950  
951-960  
961-970  
971-980  
981-990  
991-1000



**FIGURE 49**

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCTGTGTGTACCAAGAGCTGGAGACACCA  
 TCTCCACCGAGAGT**CATG**CCCCCATTGGCCCTGCACCTCCTCGTCTCGTCCCCATCCTCC  
 TCAGCCTGGTGGCCTCCAGGACTGGAAGGCTGAACGCAGGCCAAGACCCCTTCGAGAAATGC  
 ATGCAGGATCTGACTATGAGCAGCTGCTCAAGGTGGTGACCTGGGGGCTCAATCGGACCCT  
 GAAGCCCCAGAGGGTGATTGTGGTTGGCGCTGGTGTGGCCGGGCTGGTGGCCGCCAAGGTGC  
 TCAGCGATGCTGGACACAAGGTCAACATCCTGGAGGCAGATAACAGGATCGGGGGCCGCATC  
 TTCACCTACCGGGACCAGAACACGGGCTGGATTGGGGAGCTGGGAGCCATGCGCATGCCAG  
 CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCTGGGGCTCAACCTGACCAAGTTCACCC  
 AGTACGACAAGAACACGTGGACGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAG  
 AAGGTGCCCGAGAAGCTGGGCTACGCCTTGCCTCCCCAGGAAAAGGGCCACTCGCCCGAAGA  
 CATCTACCAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACTGGGCTGCAGAAAGG  
 CGATGAAGAAGTTTGAAGGCACACGCTCTTGAATATCTTCTCGGGGAGGGGAACCTGAGC  
 CGGCCGGCCGTGCAGCTTCTGGGAGACGTGATGTCCGAGGATGGCTTCTTCTATCTCAGCTT  
 CGCCGAGGGCCCTCCGGGCCACAGCTGCCTCAGCGACAGACTCCAGTACAGCCGCATCGTGG  
 GTGGCTGGGACCTGCTGCCGCGCGCTGCTGAGCTCGCTGTCCGGGCTTGTGCTGTTGAAC  
 GCGCCCGTGGTGGCGATGACCCAGGGACCGACGATGTGCACGTGCAGATCGAGACCTCTCC  
 CCCGGCGCGGAATCTGAAGGTGCTGAAGGCCGACGTGGTGTGCTGACGCGAGCGGACCGG  
 CGGTGAAGCGCATCACCTTCTCGCCGCGCTGCCCCGCCACATGCAGGAGGCGCTGCGGAGG  
 CTGCACTACGTGCCGGCCACCAAGGTGTTCTTAAGCTTCCGAGGCCCTTCTGGCGCGAGGA  
 GCACATTGAAGCGGCCACTCAAACACCGATCGCCCGTCGCGCATGATTTTCTACCCGCCGC  
 CGCGCGAGGGCGCGCTGCTGCTGGCCTCGTACACGTGGTTCGACGCGCGCGGCAGCGTTCGCC  
 GGCTTGAGCCGGGAAGAGCGTTTGGCTTGGCGCTCGACGACGTGGCGCATTTGCACGGGCC  
 TGTCTGCGCCAGCTCTGGGACGGCACCGGCGTCTCAAGCGTTGGGCGGAGGACAGCACA  
 GCCAGGGTGGCTTTGTGGTACAGCCGCCGGCGCTCTGGCAAACCGAAAAGGATGACTGGACG  
 GTCCCTTATGGCCGATCTACTTTGCCGGCGAGCACACCGCCTACCCGCACGGCTGGGTGGA  
 GACGGCGGTCAAGTCGGCGCTGCGCGCCGCCATCAAGATCAACAGCCGGAAGGGGCTGCAT  
 CGGACACGGCCAGCCCCGAGGGGCACGCATCTGACATGGAGGGGCAGGGGCATGTGCATGGG  
 GTGGCCAGCAGCCCTCGCATGACCTGGCAAAGGAAGAAGGCAGCCACCTCCAGTCCAAGG  
 CCAGTTATCTCTCAAAAACAGCCACACGAGGACCTCGCAT**TAA**AGTATTTTCGAAAAA  
 AA

**FIGURE 50**

MAPLALHLLVLVPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVVTWGLNRTLKPQRV  
 IVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRIL  
 HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPKEKLYALRPQEKGHSPEDIYQMA  
 LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSSEDGFFYLSFAEALR  
 AHSCLSDRLOYSRIVGGWDLPLRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPPARNL  
 KVLKADVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFRFPFWREEHIEGG  
 HSNTDRPSRMIFYPPREGALLASYTWSDAFAAGLSREEALRLALDDVAALHGPVVRQL  
 WDGTVVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS  
 ALRAAIKINSRKGPSDTPASPEGHASDMEGQGHVHGVASSPSHDLAKEEGSHPPVQQLSLQ  
 NTHTRTSH

**Signal peptide:**

amino acids 1-21

# FIGURE 51

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCGGCCCTTCTGCCTGCAT  
 GGACGCTCTGAAGCCACCTGTCTCTGGAGGAACACAGAGCGAGGGAAGAGGACAGGACTCGTGTGGCAGGAA  
 GAACCTCAGAGCCGGGAAGCCCCATCTACTAGAAGCACTGAGAGATGCGGCCCTCGCAGGGCTGAATTTCTCT  
 GCTGCTGTTCACAAAGATGCTTTTTTATCTTTAACTTTTTTGTCTTCCCACTCTCCGACCCCGGGCTTGATCTGCAT  
 CCTGACATTTGGAGCTGCCATCTCTTTGTGGCTGATCACCAGACCTCAACCCGCTTTACCTCTTGTGACCTGAA  
 CAATCAGTCTGTGGGAATTGAGGGAGGAGCAGCGAAGGGGGTTTCCCAAGAGCAATGACCTTAACAAAGTTGCTG  
 CTTCTCAGATGCCAAGACTATGTATGAGGTTTCCAAAGAGGACTCGCTGTCTGACAATGGGCCCTGCTTGGG  
 ATATAGAAACCAACAGCCCTACAGATGGCTATCTTACAAACAGGTGTCTGATAGAGCAGAGTACCTGGGTTCT  
 CTGCTCTTTGATCAAGGTTATAAATCATCACCAGACCACTTTGCGGCATCTTTGCTCAGAATAGGCCCAGAGTG  
 GATCATCTCCGAATTTGGCTTTGTACAGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTGGGACCAGAAGC  
 CATCTGACATATTGTCAACAAGGCTGATATGCCATGGTGATCTGTGACACACCCAAAGGCACTTGGTGGTAT  
 AGGGAATGTAGAAAAGGCTTCAACCCGAGCCTGAAGGTGATCATCCTTATGGACCCCTTTGATGATGACCTGAA  
 GCAAAGAGGGGAGAAGAGTGAAGTTGAGATCTTATCCCTATATGATGCTGAGAACCTAGGCAAGAGCACTTCAG  
 AAAACCTGTGCCTCTAGCCCAAGAACCTGAGCCTCATCTGCTTCAACAGTGGGACCACAGGTGACCCCAAAGG  
 AGCCATGATAACCCATCAAATATTGTTCAAATGCTGCCTTTCTCAAATGTGTGGAGCATGCTTATGAGCC  
 CACTCCTGATGATGTGGCCATATCTTACCTCCCTCTGGCTCATATGTTTGAGAGGATTTGATACGGCTGTTGTGTA  
 CAGCTGTGGAGCCAGAGTTGGATTCTTCCAGGGGATTTCCGTTGCTGGCTGACGACATGAAGACTTTGAAGCC  
 CACATTTGTTCCCGCGGTGCTCGACTCCTTAACAGGATCTACGATAAAGGTACAAATGAGGCCAAGACCCCTT  
 GAAGAAGTTCTGTTGAAGCTGGCTGTTTCCAGTAAATCAAAGAGCTTCAAAGGGTATCATCAGGCACTGATAG  
 TTTCTGGGACAAGCTCATCTTTGCAAAGATCCAGGACAGCCTGGGCGAAGGTTCTGTTAATTTGCTACTGGAGC  
 TGCCCCATGTCCACTTTCACTCATGACATTTCTCCGGGACAGCAATGGAGTGTGAGGTATGAGGCTTATGGTCA  
 AACAGAAATGACAGGTTGGCTGATACATTTACATTTACCTGGGACTGGACATCAGGTCAGTTGGGCTGCCCTGGC  
 TTGCAATTACGTTGAAGCTGGAAGATGTGGCTGACATGACTACTTTACAGTGAATTAAGGAGAGGCTGTGCAT  
 CAAGGGTACAAAGCTGTTCAAAGGATACCTGAAGGACCCTGAGAAGACACAGAGGAGCCTGGACAGTGTGGCTG  
 GCTTCAACACAGGAGACATTTGGTGCCTGGCTCCGCAATGGAATCTCTGAAGATCATCGACCGTAAAAAGAACATTTT  
 CAAGCTGGCCCAAGGAGAATACATTGCAACGAGAAAGATAGAAAATATCTACACAGGAGTCAACCAAGTTTACA  
 AATTTTGTACACGGGAGAGCTTACGCTCATCCTTAGTAGGAGTGTGGTTCCTGACACAGATGTACTTCCCTC  
 ATTTGACGCGAAGCTTGGGGTGAAGGGCTCCTTTGAGGAACGTGCCAAACCAAGTTGTAAAGGAAGCCATTTT  
 AGAAGACTTGCAAAAAATTTGGGAAGAAAGTGGCTTAAACCTTTTGAACAGGTCAAAGCCATTTTCTTCATCC  
 AGAGCCATTTCCATTGAAAAATGGGCTCTTGACACCAACATTTGAAGCAAAAGCAGGAGAGCTTTCCAAATACTT  
 TCGGACCCAAATTTGACAGCCTGTATGAGCACATCCAGGATAGGATAAGGTACTTAACTAAGTCACTGCCGCCCACTG  
 TGCACTGCTTGTGAGAAAAATGGATTAAAAACTATTCTTACATTTGTTTGGCTTCCCTCCTAATTTTTTTTAAACC  
 TGTAAACTCTAAAGCCATAGCTTTGTTTATATATGAGACATATAATGTGTAACCTAGTTCCCAATTAATCA  
 ATCTGTCTTTCCCATCTCGATGTGTGCTAATATTAAGGCTTCAGGGCTACTTTTATCAACATGCCTGTCTTCAA  
 GATCCGAGTTTATGTTCTGTCTTCTCTCATGATTTCCAACCTTAATACTATTAGTAACCACAAGTTCAGGGGT  
 CAAGGGGACCTCTGCTGCTCTTCTTTGTTTGTGATAAACATATGCTGCCAACAGTCTCATGTCTATTATTACA  
 TCTTCTACTGTCAAACATAAGAGATTTTAAATCTGAAAACTGCTTACAATTCATGTTTTCTAGCCACTCCAC  
 AAACCACTAAATTTAGTTTGTAGCCTATCACTCATGTCAATCATATCTATGAGACAAATGTCCCGATGCTCTT  
 CTGCGTAAATTAATTTGTACTGAAGGGAAAGTTTGATCATACCAACATTTCTCAACTCTCTAGTGTAGATA  
 TCTGACTTTGGGAGTATTAAAAATGGGTCTATGACATACTGTCCAAAGGAATGCTGTTCTTAAAGCATTTATTA  
 CAGTAGGAACTGGGAGGTAATCTGTTCCTACAGTTTGTGCTGAGCTGGAAGCTGTGGGGAGGAGGTGACA  
 GTGGGCCCACTGAACTTTCCAGTAAATGAAGCAAGCACTGAATAAAAGCCCTCTGAACTGGGAACAAAGATCT  
 ACAGGCACAGCAAGATGCCACACCAACAGGCTTATTTCTGTGAAGGAACCACTGATCTCCCCACCCTTGGATT  
 AGAGTTCTGCTGCTTACCTTACCCACAGATAACACATGTTGTTCTACTTGTAAATGTAAAGTCTTTAAATAAAC  
 TATTACAGATAAAAAA

**FIGURE 52**

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775
<subunit 1 of 1, 739 aa, 1 stop
<MW: 82263, pI: 7.55, NX(S/T): 3
MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNFLLLFTKMLFIFN
FLFSPLPTPALICILTFGAAIFLWLITRPQVPLPLDLNNQSVGIEGGARKGVSQKNNDLTS
CCFSDAKTMYEVEVFORGLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYS
PDQFVGIFAQNRPEWIISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKAL
VLIGNVEKGFTPSLKVIIIMDPFDDDLKQGEKSGIEILSLYDAENLGKEHFRKVPVPPSPED
LSVICFTSGTTGDPKGAMITHQNIIVSNAAFLKCEHAYEPTPDDVAISYLP LAHMFERIVQ
AVVYSCGARVGFFQGDIRLLADDMKTLKPTLFPAPVRLNRIYDKVQNEAKTPLKKFLLKLA
VSSKFKELOKGIIRHDSFWDKLI FAKIQDSLGGRRVRVIVTGAAPMSTSVMTFFRAAMGCQVY
EAYGQTECTGGCTFTLP GDWTS GHVGVPLACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFK
GYLKDPEKTQEALDSDGWLHTGDIGRWLPNGTLKII DRKKNIFKLAQGEYIAPEKIENIYNR
SQPVLQIFVHGESLRSSLVGVVVPD TDVLP SFAAKLGVKGSFEELCQNQVVREAILEDLQKI
GKESGLKTFEQVKAIFLHPEPF SIENGLLTPTLKAKRGELSKYFRTQIDSLYEHIQD

```

**Important features:****Type II transmembrane domain:**

amino acids 61-80

**Putative AMP-binding domain signature.**

amino acids 314-325

**N-glycosylation site.**

amino acids 102-105, 588-591 and 619-622

**FIGURE 53**

GGAGGCGGAGGCCGCGGCGAGCCGGGCCGAGCAGTGAGGGCCCTAGCGGGGCCGAGCGGGG  
 CCCGGGGCCCCTAAGCCATTCTGAAATCATGGGCTGGCCAGGACATTTGGTGACCCGCCAAT  
 CCGGTATGGACGACTGGAAGCCAGCCCTCATCAAGCCCTTTGGGGCTCGGAAGAAGCGG  
 AGCTGGTACCTTACCTGGGAAGTATAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTCA  
 GACAGGGGCCCTGCTTTCCCTGCTGGTGACTGTCAATTGTCAATATCAAGTTGATCTGGACA  
 CTCCGCGAGCCATCAGTGAAGCCAAATGAAGACCCAGAGCCAGACGACATGATGAGGCC  
 CTAGGCCGCCCTGGAGCCCCACGGGCGCAGAGGCAGTGGTCCCCGGCGGGTCTTGACGCTAGA  
 GGTGTATTCAAGTCGCGAGCAAGTATATGTGGCAGTGGATGGCACCAGCGTCTGGAGGATG  
 AGGCCCGGGAGCAGGGCCGGGGCATCCATGTCAATTGTCTCAACCAGGCCACGGGCCACGTG  
 ATGGCAAAACGTGTGTTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGCTATTCTCT  
 CAACATGGTAGCGCCCGGCCGAGTGCTCATCTGCAGTGTCAAGGATGAGGGCTCCTTCCACC  
 TCAAGGACACAGCCAAGGCTCTGCTGAGGAGCTGGGCGAGCCAGGCTGGCCCTGCCCTGGGC  
 TGGAGGGACACATGGGCCCTTCGTGGGACGAAAGGAGGTCTGTCTTGGGGAGAAACATTC  
 TAAGTCACCTGCCCTCTCTTCTGGGGGACCCAGTCTGTCTGAAGACAGATGTGCCATTGA  
 GCTCAGCAGAAGAGGCAGAGTGCCACTGGGCGACACAGAGCTGAACCGTCGCCGCCGGCGC  
 TTCTGCGACAAAGTTGAGGGCTATGGAAGTGTATGCGAGCTGCAAGGACCCACACCCATCGA  
 GTTCAGCCCTGACCCACTCCAGACAACAAGGTCTCAATGTGCTGTGGCTGTCTATTGACG  
 GGAACCGACCCAAATTACTGTACAGGATGCTGCGCTCTCTGCTTTCAGCCAGGGGGTGTCT  
 CCTCAGATGATAACAGTTTTCATTGACGGCTACTATGAGGAACCCATGGATGTGGTGCCACT  
 GTTTGGTCTGAGGGGCATCCAGCATACTCCCATCAGCATCAAGAAATGCCCGGTGTCTCAGC  
 ACTACAAGGCCAGCCTCACTGCCACTTCAACCTGTTTCCGAGGCCAAGTTTGTGTGGTT  
 CTGGAAGAGGACCTGGACATTGCTGTGGATTTTTCAGTTTCTGAGCCAATCCATCCACCT  
 ACTGGAGGAGGATGACAGCCTGTACTGCATCTCTGCCTGGAATGACCAGGGGTATGAACACA  
 CGGCTGAGGACCCAGCACTACTGTACCGTGTGGAGACCATGCCTGGGCTGGGCTGGGTGCTC  
 AGGAGGTCTTGTACAAGGAGGAGCTTGAGCCCAAGTGCCCTACACCGGAAAGCTCTGGGA  
 TTGGGACATGTGGATGCGGATGCCTGAACAACGCGGGGCCGAGAGTGATCATTCCTTGAGC  
 TTTCCCGATCTTACCCTTTGGCATCGTGGCCCTCAACATGAATGGTACTTTTACAGGAGGC  
 TACTTCAAGAAGCACAAGTTCAACACGGTTCAGGTGTCCAGCTCAGGAATGTGGACAGTCT  
 GAAGAAAGAAAGCTTATGAAGTGGAAGTTACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACC  
 ACAGCAAGAACCCTTGTGAAGACTCTTCTGCCAGACACAGAGGGCCACACCTACGTGGCC  
 TTTATTCGAATGGAGAAGATGATGACTTCACCACCTGGACCCAGCTTGCCAAAGTGCTCCA  
 TATCTGGGACCTGGATGTGCTGGCAACCATCGGGCCCTGTGGAGATTGTTTCGGAAGAAGA  
 ACCACTTCTGTGGTGGGGTCCGGCTTCCCTTACTCAGTGAAGAGCCACCCCTCAGTC  
 ACCCAATTTTCTGGAGCCACCCCCAAGGAGGAGGGGAGCCCCAGGAGCCCAAGACAGAC  
 ATGAACCTCTCCAGACCTCGGGGCTGGGTACTGTGTACCCCAAGCTGGCTAGCCCT  
 TCCCTCCATCCTGTAGGATTTTGTAGATGCTGGTAGGGGCTGGGGCTACCTTGTTTTTAA  
 TGAGACTTAATTACTAACTCAAGGGGAGGGTTCCCTGCTCCAAACCCCCGTCTCGAGTT  
 AAAAGTCTATTTTATTTTCTCTTGTGGAGAAGGCAGAGAGTACTGTGGGAATCATTACG  
 ATCCCTAGCAGCTCATCTGCCCTTTGAATACCTCACTTTCAGGCCCTGGCTCAGAACTTA  
 ACCTATTTATTGACTGTCTGAGGGCCTTGAAAAAGGCCGAACCTGGAGGGCCTGGATTTC  
 TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGCTGGCTCTTACTCAGGAACCTGCTGTGCC  
 CAACCTAGGACAGGCCAGCTGGGGCCACATGCTGACACAGACTCACTCAGAGACCCCTTA  
 GACACTGGACAGGCCCTCTCTCAGCCTTCTCTTTGTCAGATTTCCTCAAGCTGGATTAAGT  
 GGTCAATTGATTAATAAAGGAGAAGCCCTCTGGGAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 54**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185

><subunit 1 of 1, 660 aa, 1 stop

><MW: 75220, pI: 6.76, NX(S/T): 0

MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQALRRFCQTGAVLFLLVTVIVNIKLILDTR  
 RAISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDVEVYSSRSKVYVAVDGTTVLEDEA  
 REQGRGIHVIVLNQATGHVMAKRVFDTYSPHEDEAMVFLNMVAPGRVLICTVKDEGSFHLK  
 DTAKALLRSLGSQAGPALGWRDTWAFVGRKGGPVFGEKHSKSPALSSWGDVPVLLKTDVPLSS  
 AEEAECHWADTELNRRRRRFCCKVEGYGSVCCKDPTPIEFSPDPLPDKNLNVPVAVIAGN  
 RPNYLYRMLRLLSAQGVSPQMITVFIDGYEPEMDVVALFGLRGIQHTPISIKNARVSQHY  
 KASLTATFNLFPFAKFAVLEEDLDIAVDFFSFLSQSIHLLEEDDSLYCISAWNDQGYEHTA  
 EDPALLYRVETMPGLGWVLRRLSYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECIIPDVS  
 RSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDLSLKKEAYEVEVHRLLEAEVLDHS  
 KNPCEDSFLPDTEGHTYVAFIRMEKDDFTTWTQLAKCLHIWDLVVRGNHRLGLWRLFRKKNH  
 FLVVGVPASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT

**Important features of the protein:**

**Transmembrane domain:**

amino acids 38-55

**Homologous region to Mouse GNT1**

amino acids 229-660

**FIGURE 55**

CGGACGCGTGGGCTGCTGGTGGGAAGGCCATAAGAAGCTGGAAGGCCACTCTCTTGGAAACCCACAC  
 CTGTTTTAAAGAACCTTAAGCACCATTAAAGGCCACTGGAATTTGTTGCTCTAGTGGTTGTGGGGTGAATA  
 AAGGAGGGCAGAAATGGATGATTTTCATCTCCATTAGCCTGCTGTCTCTGGCTATGTTGGTGGATGTTA  
 CGTGGCCGGAATCATTCCCTTGGCTGTTAATTTCTCAGAGGAACGACTGAAGCTGGTGACTGTTTTGG  
 GTGCTGGCCTTCTCTGTGGAAGTCTCTGGCAGTCATCGTGCCTGAAGGAGTACATGCCCTTTATGAA  
 GATATTCTTGAAGGAAACACCACCAAGTGAACACATAATGTGATTGCATCAGACAAAGCAGC  
 AGAAAAATCAGTTGTCATGAACATGAGCAGGCCAGCACCACACAGCTGCATCCCTATATTTGGTG  
 TTTCCCTCGTTCTGGGCTTCGTTTTTCATGTTGCTGGTGGACAGATTGGTAACCTCCCATCTGCAATCT  
 ACTGACGATCCAGAAGCAGCAAGGCTCTAGCAATCCAAATACACCACCGCTGGGTCTGGTTGTCCA  
 TGCTGCAGCTGATGGTGTGCTTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTTAATTG  
 TGTTTTGGCAATCATGCTACATAAGGCACGAGCTGCTTTTGGACTGGTTTCCTTCTTGATGCATGCT  
 GGCTTAGAGCGGAATCGAATCAGAAAGCACTTGTGCTGCTTTGCATTGGCAGCACCAGTTATGTCAT  
 GGTGACATACTTAGGACTGAGTAAGAGCAGTAAAGAAGCCCTTCAGAGGTGAACGCCACGGGAGTGG  
 CCATGCTTTTCTCTGCCGGGACATTCTTTATGTTGCCACAGTACATGCTCCTCCTGAGGTGGCGGA  
 ATAGGGCAGCAGCAAGCCGATGCCAGGGAGGAGGCCCTCAGCCGCTGGAAGTGGCAGCCCT  
 GGTTCCTGGGTTGGCTCATCCCTCTCATCTGTCAGTAGGACACCAGCATTAAATGTTCAAGGTCCAGC  
 TTTGGTCCAGGGCCGTTTTGCCATCCAGTGAGAACAGCCGGACCGTGACAGCTACTCACTTCCTCAGTC  
 CTCTGTCTCACTTGGCATCTCTACATGTATCTTAGAGTCCAGAGGGGAGGTGAGGTTAAAAACCTG  
 AGTAATGGAAGCTTTTAGAGTAGAAACACATTTACGTTGCAGTTAGCTATAGACATCCCATTTGTGT  
 TATCTTTTAAAGGCCCTTGACATTTTGCCTTTTAATATTCTCTTAACCTTATCTCAGGGAAGATG  
 GAATTTAGTTTTAAGAAAAGAGGAGAACTTCATACTCACAATGAATAGTGATTATGAAAATACAGT  
 GTTCTGTAATTAAGCTATGCTCTTTCTTCTTAGTTTAGAGGCTCTGCTACTTTATCCATTGATTTTT  
 AACATGGTTCACCACATGTAGACTGGTGCTTTAGCATCTATGCCACATCGCTTGATGGAAGGTCATA  
 GCACCCACTCACTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGGTCAGGAAAATGATAGC  
 AAGACACATTGAAAGCTCTCTTTATACTCAAAGAGATATCCATTGAAAAGGGATGCTAGAGGGATT  
 TAAACAGCTCCTTTGGCAGCTGCCCTCTGAAATCCAGCCTGCCATCCATCAAATGGAGCAGGAGAGG  
 TGGGAGGAGCTTCTAAGAGGTTGACTGGTATTTGTAGCATTCTTGCAAGTTCTCCTTTGCAGAA  
 ACCTGTCTCCACATTTCTAGAGAGGAGCCAGTTCTAGTAGTTTCAGTTCTAGGCTTTCCTTCAAGAA  
 CAGTCAGATCACAAGTGCTCTTTGGAATTAAGGGATATTAATTTTAAGTGATTTTTGGATGGTTAT  
 TGATATCTTTGTAGTAGCTTTTTTAAAGACTACCAAATGTATGGTTGTCCTTTTTTTTTTGTTTTT  
 TTTTTTTTTTAATATTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAAATACTAGGTCAGCTTT  
 GGCACACTGTGCTTCTACATAACCACTGTAGCAAGATGGATCAAAATGAGAAGTGTTCCTTA  
 TTGATTAAAGCTTATTGGAATCATGCTCTTGTCTCTTCTGCTTTTCTTGTCTTTCTCTAATCTTT  
 TCCCTCTAGCCTCTCTCGGCCAATTTGCTGCTTACTGCTGGTGTAAATATTTGTGTGGGATGAATT  
 CTTATCAGGACAACCACTTCTCGAATGTAATAATGAAGATAATAATATCTTTATCTTTATCCCTT  
 CAAGAAATTAACCTTTTGTGTCAAATGCCGCTTTTGTGAGCCCTTAAATACCCCTCCTCATCTGTGTA  
 ATTGACACAATCACTAATCTGTGAATTTAAACAATGTAGATAGCAAAAGTGTTTAACAGACTAGGATA  
 ATTTTTTTTTTCAATTTTGCCAAATTTTTGTAAACCTGTCTTGTCAATAGGTGATAATATGTAT  
 TATTAATTTATTTTACTTTCTATACCATTTCAAACACATTACACTAAGGGGGAACCAAGACTAGTT  
 TCTTCAGGGCAGTGGACGTAGTAGTTTGTAAACAGTTTCTATGACGCATAAGCTAGCATGCCATG  
 ATTTATTTCTCTCATGAATTTGTCACTGGATCAGCAGCTGTGGAATAAAGCTTGTGAGCCCTCTGCT  
 GGCCACAGTGAGGAAAGTAGCACAATAGGATACAGTTGTATGTAGTACTGGCAACAAATGATACATA  
 TTTTACTACCAAGAGAAGGTATAGTATGGAAGTCCAATGACTTCCTGTATGGATGTTAACAGCT  
 GACTGGTGAGACTTGAGGTTTCATCTAGTCCTTCAAACTATATGGTTCCTAGATTCTCTCTGGA  
 AACTGACTTTGTCAAATAAATAGCAGATTGTAGTGTCAAAAAAA

**FIGURE 56**

MDDFISISLLSLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL  
 YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLVDQ  
 IGNSHVHSTDDPEAARSSNSKITTTLGLVVHAAADGVALGAAASTSQTSVQLIVFVAIMLHK  
 APAAFGLVSFLMHAGLERNRIRKHLVLFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML  
 FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPILISVGHQH

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 37-56, 106-122, 211-230, 240-260, 288-304



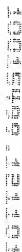
**FIGURE 57**

GCTCGAGGCCGGCGGGCGGGAGAGCGACCCGGGCGGCCTCGTAGCGGGGCCCCGGATCCC  
 CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGACATGATGGGCTTGG  
 GAAACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCCTGCATC  
 ATCGTCTTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGACCTCCAGACACGGAT  
 CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGCGCGCTGGAGCTGAAGA  
 AGAACGAGTTCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGC  
 CACAACTTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTGGTGAA  
 TAACATCACCACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCTGCAGA  
 GGAATTACGGCAGGCTGCAGCAGGATGTCTCCAGTTTCAGAAGAACCAGACCAACCTGGAG  
 AGGAAGTTCTCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG  
 TGAGGAGCGAATAGAAGAGGTCAACAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA  
 GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG  
 GCAGCAGGCTGCCACACACAGAGGTGCCACAAGGAAGGGAACGCTGCTTGGTAACAGCAA  
 GTCCAGACACCAGCCCCAGTTCGGAAGTGGTTTTGGATTCAAAGAGACAAGTTGAGAAAAG  
 AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAG  
 CCAGGCCGGGAGCAGGTGGTGAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGG  
 AGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTAGTGAGCCAGGAAAATCCAGAGA  
 TGGAGGGCCCTGAGCGAGACCAGCTTGTCATCCCCGACGGACAGGAGGAGGAGCAGGAAGCT  
 GCCGGGGAAGGGGAGAAACCAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA  
 TGAAGCAGAACTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAAACATAGATG  
 TTTTAAATGTTGAAGATCAGAAAAGAGACACCATAAATTTACTTGATCAGCGTGAAAAGCGG  
 AATCATACACTCTGAATTGAACTGGAATCACATATTTACAACAGGGCCGAAGAGATGACTA  
 TAAAATGTTTCATGAGGGACTGAATACTGAAAACGTGAAATGTACTAAATAAATGTACATCTGA

MMGLGNGRSMKS P PVL AALVACI I VLG FNYW I ASSR SVD L QTRIMELEGRV RRAA AERGA  
VELKKN EFQGELEKQREQLDKIQSSHN FQLESVN KLYQDEKAVLVNN ITTGERL RIVLQDQL  
KTLQRNYGR LQQDVLPQKQNTN LERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA  
SRDLSENN DQRQQLQALSEPQRRLQAAGLPHT E V P QGKGNVLGNSK SQT PAPSSEVVLDSKR  
QVEKEETNEI QVNVLEPQRDRLPQEAPGREQVVEDR P VGGRGFGGAGELGQT P QVQAALSVSQ  
ENPEMEGPERDQLV I PDGQEEEQEAAAGEGRNQQLRGEDDYNMDENAESETDKQAALAGND  
RNI DVFNVDEQKDRITNLDDOREKNHTL

Signal peptide:

amino acids 1-29



**FIGURE 59**

GGATG CAGAAAGCCTCAGTGTGTCTTCTCTGGCCTGGGTCTGCTTCTCTTCTACGCTGGCATTGCCCTCTTCA  
 CCAGTGGCTTCTTGCTCACCCTTTGGAGCTCACCACCATAGCAGCTGCCAAGAGCCCCAGGCCCTGGGTCCC  
 TGGCATGGGGAGCCAGGGAACCTGGGGCCTGCTGGATGGCTTCCCGATTTTCGCGGGTTGTGTGTGCTGA  
 TAGATGCTCTGGCATTTGACTTTCGCCACGCCCAGCATTACACGCTGCCATAGAGAGCTCTCTGCTCCCTACCCCT  
 TCTCGGGCAAACTAACTCCTTCGCAGAGGATCTGGAGATTGAGCCCCACCCAGCCGCTCTACCGATCTCAGG  
 TTGACCTCTTACCACCACCATGCGAGCGCTCAAGGCCCTCACCAGTGGCTCACTGCCATCTTTATTGATGCTG  
 GTAGTAACCTTCGCCAGCCACGCCATAGTGGAGACAATCTCATTAAAGAGCTCACCATTGGCAGAAGGCGTGTAG  
 TCTTCATGGGAGATGATACCTGGAAGACCTTTCCCTGGTGTCTTCCAAAGCTTTCTTCTTCCCATCTCTCA  
 ATGCTCAGAGACTAGACACAGTGGACAATGGCATCTTGGAAACCTCTACCCACCATGGACAGCTGGTGAATGGG  
 ACGTGTCTGATTGCTCACTTCTCTGGGTGTGGACCACTGTGGCCACAGCATGGGCCCTCACCACCTGAAATGGCCA  
 AGAACTTAGCCAGATGGACAGGTGATCCAGGACTTTGGAGCGCTCGGAGAATGACACACTGCTGGTAGTGG  
 CTGGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGGACAGTGAGCTGGAGTCTCAGCTGCTCTCTTTC  
 TGTATAGCCCCACAGCAGTCTTCCCCAGCAACCCACAGAGGAGCCAGAGGTGATTCTCTCAAGTTAGCCTTGTGC  
 CCACGCTGGCCCTGCTGCTGGGCCCTGCCATCCCATTTGGGAATATCGGGGAAGTATGGCTGAGCTATTCTCAG  
 GGGGTGGAGACTCCAGCCCCACTCTCTGCTTTAGCCCCAGCCTCAGCTCTCCATCTCAATGCTCAGCAGGTCT  
 CCGGATTTCTCATACTACTCAGCTGCTCCTCAGGACCTTCAAGCTAAGGAGCTTCATCAGCTGCAGAACCTCT  
 TCTCTAGGCCCTCTGCTCAGTACCAGTGGCTTCTCCAGAGCCCCAAGGGGCTGAGCGGACACTCCGCCATGTGA  
 TTGCTGAGCTCAGACGATTCTTCGGGGAGCTCGGGCCATGTGCTGAGCTCTGGGCTCGTTTCTCTCTGGTGC  
 GCATGGCGGGGGTACTGCTCTCTTGGCTGCTCCTGCTTTATCTGCTCTGCTGGCATCTCAGTGGGCAATATCCC  
 CAGGCTTTTCCATTCTGCCCTTACTCCTGACACTGTGGCCTGGGCTCGGTGGGGCCATAGCGTATGCTGGAG  
 TCTCGGGAATATTGAGCTGAAGCTAGATCTAGTGTCTTAGGGGCTGTGGCTGGAGTGAGCTATTCTCTCCCTT  
 TTCTGTGGAAAGCTCGGCTGGCTGGGGGTCCAAGAGGCCCTGGCAACCTGTTTCCCATCCCTGGGCGCTGCC  
 TGTACTCTCTGCTGTTTCGCTTGGCTGTGTCTCTCTGATAGTTTGTGTGAGCTGAGGCCAGGGCCACCCCT  
 TCCCTTTGGGCTCATTCACTCTGCTGCTGGTTGTCCAGCTTCACTGGGAGGGCCAGGCTCTTCCACTAAGCTAC  
 TCACAAATCCCCCGCTTGGCACTTCAGCCACAACAACCCCCCAGCGGCAAAATGGTGATATGCCCTGAGGCTTG  
 GAATGGGTGCTTTTATGTACAAGGCTAGCTGGGCTTTTTCATCGTTGCCCTGAAGACACACTGTTTGGCACT  
 CCTCTCCTTGCTGAGTCTCTGCGACTCCATGGTGGTGGTGGAGCCAAAGATTTATGGTATGGAGCTTGTGTGG  
 CGGCGCTGGTGAAGCTGTTAGCTCCGCTGCGCTTGTGGCTTCGCGCTATGGTAATCTCAAGAGCCCCGAGCCAC  
 CCATGCTCTTTGTGCGCTGGGAGCTGCCCTAATGGCATGGGTACTGCTGCCCTACTGGGCATTGGCGTGGGGG  
 CAGATGAGGCTCCCCCGCTCTCCGGCTCTGGTCTCTGGGGCATCCATGGTGTGCTCGGGCTAGACAGGGC  
 TGCTGCTTCAGGGCTCGGCTGCTGCTCTGGAAGCCTGTGACAGTGTGGTGAAGGCTGGGGCAGGCGCTCCAA  
 GGACCAGGACTGTCTCACTCCCTTCTCAGGCCCCCCACTTCTCAAGCTGAGTTGGATTATGTGTCCTCCAA  
 TCTACCGACATGAGAGGAGTTCGGGGGCGGTTAGAGAGGACCAATCTCAGGGTCCCCCTGACTGTGGCTG  
 CTTATCAGTTGGGGAGTGTCTACTCAGCTGCTATGGTCACAGCCCTCACCCTTTGGCTTCCCATCTCTGCTGT  
 TGGATCGGAGCGCATCAGCCTTGTGTCTGCTCTGTTTCTGACAGCTTCTTCTCTTACATCTGCTGTGCTG  
 CTGGGATACCGCTCACCACCCCTGCTCTTTTACTGTGCCATGGCAGGCTCTCGGCTTGGGCCCTCATGGCCA  
 CAGAGACCTCTACTCCACAGGCCACAGCCTGTCTTCCAGCCATCCATTGGCATGAGCCTTCGTGGGATCCC  
 CAGAGGCTCATGGCTCTGTACTTTGGCTGCTGCTTTGCTAGTGGGACCAACCTTTCGCTCCCACTCTCTCT  
 TTTCACTAGGTTGCCCACTGCTCTGCTCTGGCTTTCTCTGTGTGAGATTCAAGGGCTGGGGAGAGACAGCAGC  
 CCGGAGGATGAAGACTGATGCCAGGTGAGCCGAGGAGGAAGAGGACCTGATGGAGATGCGGCTCGGGG  
 ATCGCGCTCAGCACTCTCTAGCGACACTGCTGACGCTGGGCCCTCAAGTACCTCTTTATCCTTGGTATTGATTT  
 TGCCCTGTGCTTGGCAGCTCCATCTCTCGAGGCACTCTATGCTTGGAAAGTGTTCGCCCTAAGTTTCATAT  
 TTAGGCTGTGGGCTCATTTGTGAGCAGCGTGGGACTTCTCTGGGCTAGCTTTGGTGATGAGATGGATGGTGG  
 CTGAGCTCTGTGTTTCAAGGACTATTCTCGCCACAGCAGGCTAGCCTGATGCTGATGCTGCTGCTGCTGCTGCT  
 ACAGAGAGTGTGAGGAACAGTGTAGCTTGGCCTGTACAGGTACTGGATGATCTGCAAGACAGGCTCAGCCATCA  
 TCTTACTATCATGCTGATCCAGGGGCGCTGACATCTAGCACTTCAATTTCTATAATTCAAGACCAAGTGGAGT  
 TGATCCCTTACTCTGATTTGGATGCTCTGAGGCAAGAGGGGGCGGTCTCCGAAGTGAATAAATAGGCCCCG  
 GCGTGGTGACTTGCACCTATATCCAGCACTTTGGGAGGACAGGTTGGGAGATGCTGCTTGGTCCAGGATTC  
 AGCACGCTGTGGAACTATACAGACCCCGTCTACTATTAAAAAAGAGTGAATAAATGATAAT

**FIGURE 60**

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809
<subunit 1 of 1, 1089 aa, 1 stop
<MW: 118699, pI: 8.49, NX(S/T): 2
MQKASVLLFLAWVCFLFYAGIALFTSGFLLTRLELTNHSSCQEPGPGSLPWGSQGKPGACW
MASRFSRVVLVIDALRFDFQAQPQHSHPREPPVSLPFLGKLSLQRILEIQPHHARLYRSQ
VDPPTTMMQRLKALTGTSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRRVVFMDGDDTWKDLF
PGAFSKAFFFPFNVNRDLDTVDNGILEHLYPTMDSGEWDVLIHFLGVDHCGHKHGPHPPEM
AKKLSQMDQVIQGLVERLENDTLLVVAGDHGTTNGDHGGDSELEVSAAFLYSPTAVFPPST
PPEEPEVIPPQVSLVPTLALLGLPIPFNGNIGEVMAELFSGGEDSQPHSSALAQASALHLNAQ
QVSRFLHTYSAATQDQLQAKELHQLQNLFASKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
ARAMCIESWARFSLVRMAGGTALLAASCFICLLASQWAIISPGFPFCPLLLTPVWGLVGAI
YAGLLGTIELKLDLVLGAVAAVSSFLPFLWKAWAGWGSKRPLATLFPPIPGPVLLLLLFR
VFFSDSFVVAEARATPFLGGSFILLVVLHWEQQLLPKLLTMPRLGTSATTNPPRHNGAY
ALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPLASVMGGRAKNLWYGACVAALVALLA
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPPLRVLVSGASMVLP
RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE
EFRGRLERTKSGPLTVAAYQLGSVYSAAMVTALTLLAFPLLLLHAERISLVFLLFLQSF
LLHLAAGIPVTPGPFVTPVQAVSAWALMATQTFTYSTGHQPVPFAIHWHAAVGFPEGHGS
CTWLPALLVGANTFASHLLFAVGCPLLLWPFLCESQGLRKRQPPGNEADARVRPEEEEEEP
LMEMLRLDAPQHFYAALLQLGLKYLFIILGIQILACALAASILRRHLMVWKVFAPKFI FEAVG
FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

```

**Important features:****Signal peptide:**

amino acids 1-16

**Transmembrane domains:**

amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,  
1016-1034, 1052-1070

**Leucine zipper pattern.**

amino acids 843-864

**N-glycosylation sites.**

amino acids 37-40, 268-271

**FIGURE 61**

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCTGT  
 GTCTCTGGTGGTTTGCCATAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGA**ATGT**  
 CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT  
 TCATCACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGT  
 CCTGACAGCTCCAGAGAAGTGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAA  
 TATACTCCAATCTGAAGTATAACGTGCTGTGTTGAATACTAAATCAAACAGAACGTGGTCC  
 CAGTGTGTGACCAACCACACGCTGGTGTACCTGGCTGGAGCCGAACACTCTTTACTGCGT  
 ACACGTGGAGTCCCTTCGTCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG  
 CCAGGACTTTGAAAGATCAATCATCAGAGTTC AAGGCTAAATCATCTTCTGGTATGTTTTG  
 CCCATATCTATTACCGTGTCTTTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA  
 CGTTGGCAAAGAGAAACACCCAGCAAATTTGATTTTGATTATGGAAATGAATTTGACAAAA  
 GATTCTTTGTGCTGCTGTA**AAAAA**ATCGTGATTAACCTTATCACCTCAATATCTCGGATGAT  
 TCTAAATTTCTCATCAGGATATGAGTTTACTGGGAAAAGCAGTGATGTATCCAGCCTTAA  
 TGATCCTCAGCCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAG  
 GGATGCTTCGCATTTGATGGAAATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCT  
 CTCACCCAGCAAGAGTCCCTCAGCAGAACAATACCCCGGATAAAACAGTCATTGAATATGA  
 ATATGATGTCAGAACCACTGACATTTGTGCGGGGCCCTGAAGAGCAGGAGCTCAGTTTGCAGG  
 AGGAGGTGTCCACACAAGGAACATTATTGGAGTCGAGGCAGCGTTGGCAGTCTTGGGCCCG  
 CAAACGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCA  
 CACAGACTCGGAGGAGGGGCCGAGGAAGAGCCATCGACGACCTTGGTCGACTGGGATCCCC  
 AAACGGCAGGCTGTGTATTCCTTCGCTGTCCAGCTTCGACCAGGATTGAGAGGGCTGCGAG  
 CCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGC  
 TCCAGACAGGCCACCAGGAGAAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGGT  
 TATATGTGCAGATGGA**AAAC**TGA**TGA**GCCAACACTTCCTTTTGCTTTTGTTCCTGTGCAAC  
 AAGTGAGTCACCCCTTTGATCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTTCCAGT  
 TTGTGAGTGTCTGTGAGAATTACTTATTTCTTTCTATTCTCATAGCACGTGTGTGATTG  
 GTTCATGCATGTAGGTCTCTTAACAATGATGGTGGGCCCTCTGGAGTCCAGGGGCTGGCCGGT  
 TGTTCATGTCAGAGAAAGCAGTCAATAAATGTTGCCAGACTGGGTGCAGAATTTATTGAG  
 TGGGTGT

**FIGURE 62**

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815
<subunit 1 of 1, 442 aa, 1 stop
<MW: 49932, pI: 4.55, NX(S/T): 5
MSYNGLHQRVFKELKLLTLCSSSQIGPPEVALTTDEKSISVVLTAPKWKRNPEDLPVSMQ
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQ
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGKEKHPANLILYIGNEFD
KRFFVPAEKIVINFITLNISSDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKH
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPDPKTVIEYEDVRTDIDICAGPEEQELSL
QEEVSTQGTLLSQAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEEPSTTLVDWD
PQTGRLCIPSLSSFDQDSEGCEPSEGDGLGEEGLLSRLYEPPAPDRPPGENETYLMQFMEEW
GLYVQMEN

```

**Important features:****Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 140-163

**N-glycosylation sites.**

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

**FIGURE 63**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG  
TCTGCC**ATG**GGGCTCGGGTTGAGGGGCTGGGGACGTCCTCTGCTGACTGTGGCCACCGCCCT  
GATGCTGCCCCTGAAGCCCCCGCAGGCTCCTGGGGGGCCAGATCATCGGGGGCCACGAGG  
TGACCCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGGCCAACATCACTGCGGA  
GGCTTCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCCACTGCTTCAGCCACAGAGACCT  
CCGCACTGGCCTGGTGGTGTCTGGGCGCCACGTCTGAGTACTGCGGAGCCCAACCAGCAGG  
TGTTTGGCATCGATGCTCTCACCACGCACCCCGACTACCACCCCATGACCACGCCAACGAC  
ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCCTGGGCCCTGCAGTGGGGCTGCTGAGGCT  
GCCAGGGAGAAGGGCCAGGCCCCCAAGCGGGGACACGGTGCCGGGTGGCTGGCTGGGGCT  
TCGTGTCTGACTTTGAGGAGCTGCCGCCTGGACTGATGGAGGCCAAGGTCCGAGTGTGAGC  
CCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGCAG  
TGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCTGGTGTGCAGGA  
ACCGGGCTCACGGCCTCGTTTCTCTCGGGCCTCTGGTGCGGCGACCCCAAGACCCCGAC  
GTGTACACGCAGGTGTCCGCCTTTGTGGCCTGGATCTGGGACGTGTTTCGGCGGAGCAGTCC  
CCAGCCCGGCCCTGCTGGGACCACAGGCCCCAGGAGAAGCCGCC**TGA**GCCACAACCT  
TGCGGCATGCAAATGAGATGGCCGCTCCAGGCTGGAATGTTCCGTGGCTGGGCCCCACGGG  
AAGCCTGATGTTTCAGGTTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACATGCA  
AAGGGCAGAAGCAAACCCAGTAAATGTAACTGACAAAAAAAAAAAAAAAAAAGAA

**FIGURE 64**

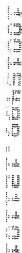
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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPYMASVRFGGQHHCGGF
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEPQQVFGIDALTTHPDYHPMTHANDIC
LLRLNGSAVLGPAVGLLRLLPGRRARPPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD
VCNSSWKGHLLTLMLCSTRSGDSHRRGFC SADSGGPLVCRNRAHGLVSFSGLWCGDPKTPDVY
TQVSAFVAWIWDVVRSSPQPGPLPGTTRPPGEAA

```

**Signal peptide:**

amino acids 1-30





**FIGURE 65**

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCCTGACGCCTGA  
 CGCCTGTCCCCGGCCCGGCATGAGCCGCTACCTGTGCGCGCTGTCGGCGCTGGGCACGGTAG  
 CAGGCGCGCCGTGCTGCTCAAGGACTATGTACCGGTGGGGCTTGCCCCAGCAAGGCCACC  
 ATCCTTGGAAGACGGTCACTGTGACGGGCGCAACACAGGCATCGGGAAGCAGACCGCCTT  
 GGAAGTGGCCAGGAGAGGAGGCAACATCATCCTGGCCTGCCGAGACATGGAGAAGTGTGAGG  
 CGGCAGCAAAGGACATCCGCGGGGAGACCTCAATCACCATGTCAACGCCCGGCACCTGGAC  
 TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGACAGAAAGATCATTGAAGAGGAGGAGCGAGT  
 GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCCCTGGACCACCGAGGACGGCT  
 TCGAGATGCAGTTTGGCGTTAACCACCTGGGTCACTTTCTCTTGACAACTTGCTGCTGGAC  
 AAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCGTCCCTGGGCCATGTTGCTGG  
 GCACATAGACTTTGACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAAGCCGCCTACT  
 GCCAGAGCAAGCTCGCCATCGTCTCTTACCAAGGAGCTGAGCCGGCGGCTGCAAGGCTCT  
 GGTGTGACTGTCAACGCCCTGCACCCGGCGTGGCCAGGACAGAGCTGGGCAGACACAGGG  
 CATCCATGGCTCCACCTTCTCCAGCACCACACTCGGGCCCATCTTCTGGCTGCTGGTCAAGA  
 GCCCCGAGCTGGCCGCCCAGCCAGCACATACCTGGCCGTGGCGGAGGAAGTGGCGGATGTT  
 TCCGGAAGTACTTCGATGGACTCAAACAGAAGGCCCCGGCCCCGAGGCTGAGGATGAGGA  
 GGTGGCCCGGAGGCTTTGGGCTGAAAGTGCCCCGCTTGGTGGGCTTAGAGGCTCCCTCTGTGA  
 GGGAGCAGCCCCCTCCCGAGATTAAACCTCTGGAGCAGATTGAAAGCCAGGATGGCGCCTCCAG  
 ACCGAGGACAGCTGTCCGCCATGCCCGCAGCTTCCTGGCACTACCTGAGCCGGGAGACCCAG  
 GACTGGCGGCCGCCATGCCCGCAGTAGGTTCTAGGGGGCGGTGCTGGCCGAGTGGAAGTGGC  
 CTGCAGGTGAGCACTGCCCGGGCTCTGGCTGGTTCGGTCTGCTCTGCTGCCAGCAGGGGAG  
 AGGGGCCATCTGATGCTTCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC  
 TGTGCACTTGCAGGCCACGTGAGGAGAGCCAGCGGTGCCTGTGCGGGAGGGTTCCAAGGTGC  
 TCCGTGAAGAGCATGGGCAAGTTGTCTGACACTTGGTGGATTCTTGGGTCCCTGTGGGACCT  
 TGTGCATGCATGGTCCTCTCTGAGCCTTGGTTTCTTACGAGTGAGATGCTCAGAATAACTG  
 CTGCTCCCATGATGGTGTGGTACAGCGAGCTGTGTCTGGCTATGGCATGGCTGTGCCGGG  
 GGTGTTTGTGTAGGGCTTCCTGTGCCAGAGCCCAGCCAGAGAGCAGGTGCAGGTGTATCCC  
 GAGTTCAGGCTCTGCACGGCATGGAGTGGGAACCCACCAGCTGCTGTACAGGACCTGGGA  
 TTGCCTGGGACTCCCACCTTCCTATCAATTCTCATGGTAGTCCAAACTGCAGACTCTCAAC  
 TTGCTCATTT

**FIGURE 66**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842
><subunit 1 of 1, 331 aa, 1 stop
><MW: 35932, pI: 8.45, NX(S/T): 1
MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERVDILINN
AGVMRCPHWTTEDGFEMQFGVNH LGHFLLTNLLLDK LKASAPSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAAYCQSKLAIVLFTKELSRRLQSGVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGPIFWLLVKPELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAEAEDEEVARRLW
AESARLVGLEAPSVREQPLPR
```

**Signal peptide:**

amino acids 1-17

**FIGURE 67**

GAAGTTCGCGAGCGCTGGCATGTGGTCTCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTG  
 GCGCTCGGGACAGGAGACCCAGAAAGGGCTGCGGCTCGGGGCGACAGGTTCTCGGGCGCTGAC  
 CAGCGTGGCGCGCGCCTGGCGCCGAGCGCGGCTGCTGGGGCTGCTGAGGCGGTACCTGC  
 GCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAGGTACTTTCTTTGCTAT  
 GAGGATTCACAAACCCCTGTGGCTAACCCCTGCTTGCATTTACTCTCATCAAACGCCGTCA  
 GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG  
 ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGG  
 GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCCTGGCCCGAGGTTGTCTT  
 TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAAACGGCTCTTTCTCTCA  
 CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACATGGGGATTATTACCATGCC  
 ATTCATGGCTGGAGGAGGCTGTCACTCTCTCCGAGGATCTTACGGAGAGTGGAAGACAGA  
 GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCGAGGAA  
 ATGTTTCGTGTGCCCTCAGCCTCTCTCGGAGTTTCTTCTCTACAGCCAGATATAAGAGG  
 ATGGCCAGGAATGTCTTGAATATGAAAGGCTCTTGGCAGAGAGCCCCAACACGTGGTAGC  
 TGAGGCTGTCTCCAGAGGCCCCAATATACCCACCTGCAGACCAGAGACCTACGAGGGGC  
 TATGTACAGCCCTGGGTTCCCAGCCCCTCTCTACAGATCCCTAGCCTCTACTGTTCCCTAT  
 GAGACCAATTCACACGCTTACCTGCTGCTCCAGCCATCCGGAAGGAGGTGATCCACCTGGA  
 GCCCTACATTGCTCTCTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAATTAGAGAAC  
 TTGCAGAACCATGGCTACAGAGGTCAGTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAG  
 TACCGCATCAGCAAAAGTGCCCTGGCTGAAGGACACTGTTGACCCAAAACCTGGTGACCCCTCAA  
 CCACCGCATTTGCTGCCCTCAGGCGCTTGATGTCCGGCCTCCCTATGCAGAGTATCTGCAGG  
 TGGTGAACATATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATGCTACGTCACCAAGC  
 AGCCCCCTCTACAGAAATGAAGTCAGGAACCGAGTTGCAACATTTATGATCTATCTGAGCTC  
 GGTGGAAGCTGGAGGAGCCACAGCCTTCACTATGCCAACCTCAGCGTGCCCTGTGGTTAGGA  
 ATGCAGCACTGTTTTGGTGGAACTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT  
 GCTGGCTGTCTGTCTCTGGTGGGAGATAAGTGGTGGCCAACAGTGGATACATGAGTATGG  
 ACAGGAATTCGCGAGCCCTGCAGCTCCAGCCCTGAAGACTTGAACTGTTGGCAGAGAGAAGC  
 TGGTGGAGTCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTAGGAGAGGAGAA  
 AGCAGAGCAGCCTCCTGGAAGAAGGCCTTGTGAGCTTTGTCTGTGCCCTCGCAATCAGAGGC  
 AAGGAGAGGTTGTTACAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAA  
 GTCAGAGTAGGATGCACAGTACAAGGAGGGGGAGTGGAGGCCGTGAGAGGGAAGTTTCTGG  
 AGTTTCAGATACTCTCTGTTGGGAACAGGACATCTCAACAGTCTCAGGTTGCATCAGTGGGTC  
 TTTTGGCACTTTGAACTTTGACCAAGGACCAAGAGTGGCAATGAGGACACCTCGAGGAG  
 GGGTAGCTGACTCCAGAACTTAAAGACTTTCTCCCACTGCTTCTGCTGCAGCCCAAG  
 CAGGGAGTGTCCCCCTCCAGAAAGCATATCCAGATGAGTGGTACATTTATATAGGATTTTT  
 TTTAAGTTGAAAACAACCTTTCTTTCTTTTGTATGATGGTTTTTAAACAGCTCATTAAAA  
 ATGTTTATAAATCAAAA

MGPGARLAALLAVLALGTGDPERAAAGDTFSALTSVARALAPERRLGLLRRYLGEEARL  
RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLASENIRALKDGYEKFV  
QDLPAFEDLEGAARMLRQDVYMLNVKGLARGVFQRTGSAITDLYSPKRLFSLTGDDCFQ  
VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRAGNVSCALS  
LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNIPHLQTRDTYEGLCQTLS  
QPTLYQIPSLYCSYETNSNAYLLLPQIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPLWQ  
RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVLTNHRIAALTGLDVRPPYAEYLQVNVYIG  
GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSEAGGATAFIYANLSVPVVRNAALFWW  
NLHRSGEGSDSLTHAGCPVLVGDKWVANKWIHEYGOEFRPCSSPED

Signal peptide:

amino acids 1-19

**FIGURE 69**

GAGATAGGGAGTCTGGGTTTAAAGTTCCTGCTCCATCTCAGGAGCCCCTGCTCCCACCCCTAG  
 GAAGCCACCAGACTCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC  
 ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGAGCCCCCGTAACCCGCGCGGGGAG  
 CGCCAGGATGCGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC  
 TGGCTCAAGTTTTCACTTATCATCTATTCCACCGTGTTCTGGCTGATTGGGGCCCTGGTCTT  
 GTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCTTGAAAGTGCCTTCC  
 TGGCTCCAGCCATCATCTCATCTCCTCTGGGCGTCGTCATGTTTCATGGTCTCCTTCATTGGT  
 GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTATGTACATCCTTGGGAT  
 CTGCCTCATCATGGAGCTCATTTGGTGGCGTGGTGGCCTTGACCTTCCGGAACCAGACCATTG  
 ACTTCTGAACGACAACATTGGAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAAA  
 AACATCATGGACTTTGTTCAGAAAAAGTTCAAGTGCTGTGGCGGGGAGACTACCGAGATTG  
 GAGCAAGAATCAGTACCAGACTGCAGTGCCCTGGACCCCTGGCCTGTGGGGTGCCCTACA  
 CCTGCTGCATCAGGAACGACAGAAAGTTGTCAACACCATGTGTGGCTACAAAATATCGAC  
 AAGGAGCGTTTCAGTGTGCAGGATGTCTACGTGCGGGGCTGCACCAACGCCGTGATCAT  
 CTGGTTCATGGACAACCTACACCATCATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCAGT  
 TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGTGGAGGACATCATCATGGAGCAC  
 TCTGTCACTGATGGGCTCCTGGGGCCCGGTGCCAAGCCAGCGTGGAGGCGGCAGGCACGGG  
 ATGCTGCTTGTGCTACCCCAATTAGGGGCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC  
 TGGGATAGACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCTCTGCCACA  
 CTCAGTACTGACCAAGCCAGGGCTGTGTGTGCTGTGTGTAGTCCCACGGCCTCTGCCCTC  
 CCCAGGGAGCAGAGCCTGGGCCTCCCCTAAGAGGCTTCCCCGAGGCAGCTCTGGAATCTGT  
 GCCACCTGGGGCTGGGGAACAAGGCCCTCCTTCTCCAGGCCTGGGCTACAGGGGAGGGA  
 GAGCCTGAGGCTCTGCTCAGGGCCATTTTCATCTCTGGCAGTGCCCTTGGCGGTGGTATTCAA  
 GGCAGTTTTGTAGCACTGTAATTGGGGAGAGGGAGTGTGCCCTTCGGGGCAGGAGGGAAGG  
 GCATCTGGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCATGGCCAGGTTGGC  
 CTCTTCTCAGCCTCCCAGGTGCCCTTGAGCCCTCTGCAAGGGCGGCTGCTTCCTTGAGCCTA  
 GTTTTTTTTTACGTGATTTTTGTAAACATTCATTTTTTTGTACAGATAACAGGAGTTTCTGAC  
 TAATCAAAGCTGGTATTTCCCGCATGTCTTATTCTTGCCCTTCCCCAACCGATTGTGTTAA  
 TCAACAATAAAAAACATGTTTTGTTTTGTTTTTAAAAA

**FIGURE 70**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863  
><subunit 1 of 1, 294 aa, 1 stop  
><MW: 33211, pI: 5.35, NX(S/T): 3  
MPRGDSEQVRYCARFSYLWLKFSLLIYSTVFWLIGALVLSVGIYAEVERQKYKTLES AFLAP  
AIIILLGVVMFMVSFIGVLASLRDNLVLLQAFMYILGICLIMELIGGVVALTRNQITIDFL  
NDNIRRGIE NYDDLD FKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPTCC  
IRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAVI IW FMDNYTIMACILLGILLPQFLG  
VLLTLLYITRVEDIIMEHSVTDGLLGPAKPSVEAAGTGCCLCYPN

**Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 22-42, 57-85, 93-116, 230-257

**FIGURE 71**

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCATTGCTGCCCTCTGA  
 CACCTGGGAAGATGCGCGGCCCGTGGACCTTCACCCTTCTCTGTGGTTTGTCTGGCAGCCACC  
 TTGATCCAAGCCACCCTCAGTCCCACTGCAGTTCTCATCCTCGGCCCAAAAGTCATCAAAGA  
 AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCTTGCAGCAGCTGCCGCTGC  
 TCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACC  
 GTCCTGAAGCACATCATCTGGCTGAAGTGCATCACAGCTAACATCCTCCAGCTGCAGGTGAA  
 GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA  
 ACACGCCCTGGTCAAGACCATCGTGGAGTTCACATGACGACTGAGGCCCAAGCCACCATC  
 CGCATGGACACCAGTGCAAGTGGCCCCACCCGCTGGTCCCTCAGTGACTGTGCCACCAGCCA  
 TGGGAGCCTGCGCATCCAAGTGTGTATAAGCTCTCCTTCTGGTGAACGCCTTAGCTAAGC  
 AGGTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTGTCCCGTG  
 ATCGAGGCTTCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCCATTTT  
 CCTCAGCATTGACCGTCTGGAGTTTACCTTCTGTATCCTGCCATCAAGGTGACACCATT  
 AGCTCTACCTGGGGCCAAGTTGTTGGACTCACAGGAAAGGTGACCAAGTGGTTCAATAAC  
 TCTGCAGCTTCCCTGACAATGCCCAACCCTGGACAACATCCCGTTAGCCTCATCGTGAGTCA  
 GGACGTGGTGAAAGCTGCAGTGGCTGCTGTGCTCTCCAGAAGAATTATGGTCTGTGGTGG  
 ACTCTGTGCTTCTTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAAG  
 GCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTT  
 TTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGTGGAAGTGTTCCCTCCA  
 GTGAAGCCCTCCGCCCTTGTTCACCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTAC  
 ACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTGAT  
 GAACTCTGGGATTGGCTGGTTCACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC  
 ACTCATCTCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCAATTGGTG  
 AAGGCCTTGGGATTGAGGCAGCTGAGTCTCTACTGACCAAGGATGCCCTTGTGCTTACTCC  
 AGCCTCCTTGTGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAG  
 GGAAGGCTGGGTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT  
 CAATAAACACTTGCTGTGAAAA

**FIGURE 72**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDNATSILQQLPLLSAM
REKPAGGIPVLGSLVNTVLKHHIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDITQLYL
GAKLLDSQGKVKWFNNSAASLTMPITLDNIPFSLIVSQDVVKAAVAVALSPPEEFMVLLDSVL
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEAL
RPLFTLGIEASSEAQFYTKGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEI IHSIL
LPNQNGKLRSGVPVSLVKALGFEEAESSLTKDALVLTPASLWKPPSPVVSQ
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 48-51, 264-267, 401-404

**Glycosaminoglycan attachment site.**

amino acids 412-415

**LBP / BPI / CETP family proteins.**

amino acids 407-457



**FIGURE 73**

GAGCGAACATGGCAGCGCGTTGGCGGTTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTG  
 CTCATCGTTTGCACGTTCCCTCAGCCTCTGCCCAAAGAAAGAGGAGATGGTGTTATCTGA  
 AAAGGTTAGTCACTGATGGAAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA  
 AGTTCCGTGCGCTTGTGAAAGCCCCACCAGAGAAATTACTCCGTTCATCGTCATGTTCACTGCT  
 CTCCAAGTGCATAGACAGTGTGTCGTTTGCAAGCAAGCTGATGAAGAATCCAGATCCTGGC  
 AAACCTCTGGGCATACTCCAGTGCATTACCAACAGGATATTTTTGCCATGGTGGATTTTG  
 ATGAAGGCTCTGATGTATTTAGATGCTAAACATGAATTCAGCTCCAACCTTTCATCAACTTT  
 CCTGCAAAAGGGAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGGTTTTTCAGC  
 TGAGCAGATTGCCCGGTGGATCGCCGACAGAAGCTGATGTCATATTTAGAGTGATTAGACCCC  
 CAAATTATGCTGGTCCCTTATGTTGGGATTGCTTTTGGCTGTTATTTGGTGGACTTGTGTAT  
 CTTGGAAGAAGTAATATGGAATTTCTCTTTAATAAAACTGGATGGGCTTTTGCAGCTTTTGTG  
 TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCCC  
 ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCAGTTTGTA  
 GCTGAAACACACATTGTTCTTCTGTTTAAATGGTGGAGTTACCTTAGGAATGGTGCTTTTATG  
 TGAAGCTGCTACCTCTGACATGGATATTGGAAGCGAAAGATAATGTGTGTGGCTGGTATTG  
 GACTTGTTGTATTTCTTCACTGGATGGATGCTCTCTATTTTTAGATCTAAATATCATGGCTAC  
 CCATACAGCTTTTCTGATGAGTTAAAAAGGTCCCAGAGATATATAGACACTGGAGTACTGGAA  
 ATTGAAAACGAAAATCGTGTGTGTTTGAAGAAGAAATGCAACTTGTATATTTTGATTAC  
 CTCTTTTTTCAAGTGATTTAAATAGTTAATCATTTAACCAAGAAGATGTGTAGTGCCTTA  
 ACAAGCAATCCTCTGTCAAAATCTGAGGTATTTGAAAATTAATTCCTCTTAACCTTCTCTT  
 CCCAGTGAACCTTATGGAACATTTAATTTAGTACAATTAAGTATATATATAAAATTTGAAAA  
 CTACTACTTTGTTTTAGTTAGAACAAGCTCAAACTACTTTAGTTAACTTGGTCATCTGAT  
 TTTATATTGCCTTATCCAAGATGGGGAAGTAAGTCTGACCAGGTGTCCACATATGCC  
 TGTTACAGATAACTACATTAGGAATTCATTCTTAGCTTCTTCATCTTTGTGTGGATGTGTAT  
 ACTTTACGCATCTTTCTTTTGGAGTAGAGAAATTAATGTGTCTCATGTGGTCTTCTGAAAAATG  
 GAACACCATTCTTTCAGAGCACACGTCTAGCCCTCAGCAAGACAGTTGTTTCTCCTCCTCCTT  
 GCATATTTCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA  
 TCTCTAAATACAGGATTATAATTTCTGCTTGAGTATGGTGTAACTACCTTGTATTTAGAAA  
 GATTTAGATTTCATTCCATCTCCTTAGTTTCTTTTAAGGTGACCCATCTGTGATAAAAAATA  
 TAGCTTAGTGCTAAAATCAGGTAACTTATACATGGCCTAAAATGTTTCTACAAATTAGAGT  
 TTGTCACTTATTCATTTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG  
 CCAGGCGCAGTGACTTACGCCTGTAATCTCAGCACTTTGGGAGGCCAAGGCAGGCAGTAC  
 GAGGTGAGGAGTTGAGAGCCATCCTGGCCAAACATGGTGAAACCCCGTCTCTACTAAAAATAT  
 AAAAAATAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCAGCTACACAGGAGGCTGAGGCAC  
 GAGAATCACTTGAACCTAGGAGATGGAGGTTTTAGTGAGCCGAGATCAGCCACTGCACTCC  
 AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAAAAA

**FIGURE 74**

MAARWRFWCVSVTMVVALIVCDVPSASAQRKKEMVLSEKVSQIMEWTNKRVPVIRMNGDKFR  
 RLVKAPPRNYSVIVMFTALQLHRQCVCVKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEG  
 SDVFQMLNMNSAPTFINFPAGKGPGRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY  
 AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN  
 PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTILGMVLLCEAATSDMDIGKRKIMCVAGIGLV  
 VLFFSWMLSIIFRSKYHGYPYSFLMS

**Signal peptide:**

amino acids 1-29

**Transmembrane domains:**

amino acids 183-205, 217-237, 217-287, 301-321

[illegible]

**FIGURE 76**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885

<subunit 1 of 1, 536 aa, 1 stop

<MW: 61450, pI: 9.17, NX(S/T): 7

MLLLWVSVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFSFGRLTFHPGSQVVKLPFFINF  
 MKTRGTSFLNAYTNSPICCPSSRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ  
 KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPMVNLIRNRTKVRVMERDWQNTDKAVNW  
 LRKEAINYTEPFVIYLG LNLPHYPSPSSGENFGSSFTHTSLYWLEKVS HDAIKI PKWSPLS  
 EMHPVDYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIIY  
 SSDHGELAMEHRQFYKMSMYEASAHVPLLMMPGIGKAGLQVSNVSVSLVDIYPTMLDIAGIPL  
 PQNLSGYSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYS DGAS  
 ILPQLFDLSSDPDEL TNVAVKFPEITYSLDQKLHSI INYPKVSASVHQYNKEQFIKWKQSIG  
 QNYSNVIANLRWHQDWQKEPRKYENAI DQWLKTHMNPRAV

**Important features:**

**Signal peptide:**

amino acids 1-15

**N-glycosylation sites.**

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,  
 498-501

**Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97

**FIGURE 77**

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG  
 AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATG**  
 GCCTCTCTTGGCCTCCAACTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACT  
 GGTGGCCATGCTGCTCCCCAGCTGGAAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAG  
 CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCAGCCAG  
 TGTGACATCTATAGCACCTTCTGGGCCTGCCCGCTGACATCCAGGCTGCCAGGCCATGAT  
 GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA  
 CAGTCTTCTGCCAGGAATCCCAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTC  
 ATCCTTGGAGGCCTCCTGGGATTCACTCCTGTTGCCCTGGAATCTTCATGGGATCCTACGGGA  
 CTTCTACTCACCCTGGTGCCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGG  
 GCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCTGCTCATCC  
 CAGAGAAATCGCTCCAATACTACGATGCCTACCAAGCCCAACCTCTGCCACAAGGAGCTC  
 TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCTACAGCCTGACAGGGT  
 ATGTG**TGA**AGAACCAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAG  
 CACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCTGAGG  
 ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGCTAGTGTAAACAGCATG  
 CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTC  
 CCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGG  
 ATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCACTG  
 ACTGACCCTCTGTGATCAAAGACCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGG  
 GGATGGGAAGGAGAAGCAGTGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC  
 TCCAAGAAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTCC  
 AGACTAATTTGTGCATGAACTGAAATAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG  
 GATGCAGGATGGGAGGACAGGAGGCAGCCTGGGACATTTAAAAAATA

**FIGURE 78**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886
><subunit 1 of 1, 230 aa, 1 stop
><MW: 24549, pI: 8.56, NX(S/T): 1
MASLGLQLVGYYLGLLGLLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT
QCDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIIISVGMRICTVFCQESRAKDRVAVAGGVF
FILGGLLGFIPIVAVNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCS
SQRRNSNYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV
```

**Important features of the protein:****Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59

**FIGURE 79**

GCACTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCC**ATG**GTGCCCAGAATCTTCGCTCCTGC  
 TTATGTGTCACTGTCTCCTCCTCTTGTGTCCAAGGAAGTCATCGCTCCCGCTGGCTCAG  
 AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAG  
 TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCTGCAC  
 CTTCTGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCTTTGGCCTCACAAACGATTTTGTG  
 TGAAGCTGAAGGTTCAAGGTGTGAATCCCAGTGCCACTCATCTCCCATCTCCAGTAAATGT  
 GAAAGCAGAAGACGTTTTCCCT**TGA**GAAAGACATAGAAAGAAAATCAACTTTCACTAAGGCATC  
 TCAGAAACATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATG  
 ATGCAGCTCCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT  
 AGATTATCAGGAAATAAATAAAGTGTTTTTCCAATGTACACACCTGTAAA

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**FIGURE 80**

MVPRIFAPAYVSVCLLLCPREVIAPAGSEPWLCQPAPRCGDKIYNPLEQCCYNDAIVSLSE  
 TRQCGPPCTFWPCFELCCLDSFGLTNDFFVVKLVQGVNSQCHSSPISSKCESRRRFP

**Signal peptide:**

amino acids 1-25

1-25  
 26-50  
 51-75  
 76-100  
 101-125  
 126-150  
 151-175  
 176-200  
 201-225  
 226-250  
 251-275  
 276-300  
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 751-775  
 776-800  
 801-825  
 826-850  
 851-875  
 876-900  
 901-925  
 926-950  
 951-975  
 976-1000



**FIGURE 81**

CTCCACTGCAACCACCCAGAGCCCATGGGCTCCCCGAGGCTGCATCGTAGCTGTCCTTTGCCATT  
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT  
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCTGCAGCACTGTT  
GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGAGCTGTGGAAACTGCACCTTCAGA  
GTCTGCTTTGAGCAGTGCTGCCCTGGACCTTCATGGTGAAGCTGATAAACAGAACTGCGA  
CTCAGCCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTCACTTAATGGAACATCAGGGGAA  
CGATGACTCCTGGATTCTCCTTCCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTTACCTGAGA  
TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACTCAACTGCCCACTTCATT  
CTGTGACCTGTCTGAGGCCACCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTTCTAG  
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCTCCTGAT  
GACCCCTATGGCCAACATCAACCCGGCACCACCCCAAGGCTGGCTGGGGAACCTTCACCCCT  
TCTGTGAGATTTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAA  
TAAATTTATGTACTTTATAAATGAAAA

**FIGURE 82**

MAPRGCI VAVFAIFCISRL L CSHGAPVAPMT PYLMLCQPHKRCGDKFYDPLQHCCYDDAVVP  
LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCDSARTSDDRLCRSVS

**Signal peptide:**

amino acids 1-24

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**FIGURE 83**

GGGGGGGGGTGCCTGGAGCAGGCGCTGGGGCCGCCCCGAGCGCTCACTCGCTCGCACTCAG  
 TCGCGGGAGGCTTCCCCGCGCCGCGCGCTCCCGCCGCTCCCCGGCACCAGAAATTCCTCT  
 GCGCGTCCGACGGCGACATGGGCGTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA  
 TCCCTGCTCTTCGCTCTCTCTCTGGCTGCGTCCCTAGGTCGGGTGGCAGCCTTCAAGGTGCG  
 CACGCCGTATTCCTGTATGTCTGTCCGAGGGGCGAAGCTCACCTCACCTGCAGGCTCT  
 TGGGCCCTGTGGACAAAGGGCAGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG  
 GCGAGGTGCAGACCTGCTCAGAGCGCCGCCCCATCCGCAACCTCACGTTCCAGGACCTTCA  
 CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC  
 TGGAGTCGGCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCCTGCTG  
 GATAGCGGCTCTACTGCTGCTGGTGGTGGAGATCAGGCACCACCCTCGGAGCACAGGCT  
 CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAACCTGTGTGGTGT  
 ACCCATCCTCCTCCAGGATAGTGAAAAATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC  
 ATCGTAGGAATCCTCTGCCTCCCCCTCATCTGCTCTGGTCTACAAGCAAAGGCAGGCAGC  
 CTCCAACCGCGTGCCAGGAGCTGGTGGGATGGACAGCAACATTCAAGGGATTGAAAACC  
 CCGGCTTTGAAGCCTCACACCTGCCAGGGGATACCGAGGCCAAAGTCAGGCACCCCTG  
 TCCATGTGGGCCAGCGGCAGCCTTCTGAGTCTGGCGGGCATCTGCTTTCGGAGCCAGCAC  
 CCCCCTGTCTCCTCCAGGCCCGGAGAGCTCTTCTTCCATCCTTGACCTGTCCCTGACT  
 CTCAAACCTTTGAGGTCACTTAGCCCAGCTGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG  
 GGCAGGTGCATTGAGCCAGGGCTGGCTCTGTGAGTGGCCTCCTTGCCCTCGGCCCTGGTTC  
 CCTCCCTCCTGCTCTGGGCTCAGATACTGTGACATCCAGAAGCCAGCCCTCAACCCCTC  
 TGGATGCTACATGGGATGCTGGACGGCTCAGCCCTGTTCCAAGGATTTTGGGGTCTGAG  
 ATTCTCCCTAGAGACCTGAAATTCACAGCTACAGATGCCAAATGACTTACATCTTAAGAA  
 GTCTCAGAACGTCCAGCCCTTCAGCAGCTCTCGTCTGAGACATGAGCCTTGGGATGTGGCA  
 GCATCAGTGGGACAAGATGGACACTGGGCCACCCTCCAGGCACCAGACACAGGGCACGGTG  
 GAGAGACTTCTCCCCGTGGCGCCTTGGCTCCCCCGTTTGGCCGAGGCTGCTCTCTGTG  
 AGACTTCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCCTGCCCACTGGCCATCGCC  
 ACCTTCCCAGCTGCCTCTACACAGCTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT  
 CTGGGGCTTCCACTGCCTGCATTCCAGTCCCAGAGCTTGGTGGTCCCGAAACGGGAAGTAC  
 ATATTGGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTTGGGCAATCTGAGGCCAGGACAG  
 ATGTTGCCCCACCCACTGGAGATGGTGTGAGGGAGGTGGTGGGGCCTTCTGGGAAGGTGA  
 GTGGAGAGGGGCACCTGCCCCCGCCCTCCCCATCCCTACTCCCACTGCTCAGCGCGGGCC  
 ATTGCAAGGGTGCCACACAATGTCTTGTCCACCTGGGACACTTCTGAGTATGAAGCGGGAT  
 GCTATTAATACTACATGGGGAAAAAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

**FIGURE 84**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897
><subunit 1 of 1, 311 aa, 1 stop
><MW: 33908, pI: 6.87, NX(S/T): 6
MGVPTALEAGSWRWGSLFLAASLGPVAAFVATPYSLYVCPEGQNVTLTCRLLGVPDK
GHDVTFYKTWYRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLESASD
HHGNFSITMRNLTLDDSGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNVCVYPSSSQ
DSENITAAALATGACIVGILCLPLILLVYKQQAASNRRAQELVRMDSNIQGIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPFPGGDVFFPSLDPVPDSPNFEVI
```

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 190-216

**FIGURE 85**

CCCACGCGTCCGCGCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCT  
 TTCCCCGCGTTCTCTTTCCACCTTTTCTCTTCTTCCACCTTAGACCTCCCTTCTGCCCCTCC  
 TTTCTTCCCCACCGCTGCTTCTGCGCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGG  
 GGTCTGTGGGTGATCTGTGGCCCCGTGCCTCCGTGTCTTTTCGTCTCCCTTCTCCCGA  
 CTCGCTCCCCGACCAGCGGCCGTGACCTGGGGAAGGATGGTTCCCGAGGTGAGGGTCTC  
 TCTCTTGTGTGGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCACGCTCGAGCCGCC  
 AGACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCTACT  
 TGGAGCCACAAGGCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGT  
 TGTACCGCTCCACTGTCCGCTGTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATG  
 CTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCCCACCAAGTCTGCC  
 AGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCCTCC  
 CGCTGCCCCAACAGTGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCCTCAC  
 AACCTGCCCCGAACCAGGCTGCCAGCACCCCTCCCCTGCCAGACTCCTGCTGCCAAGCCT  
 GCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTG  
 AGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGGGCACCCAGC  
 CCCCCTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCAAGGGAGCAG  
 GCAGCACAACGTGCAAGATCGTCTGAAGGAGAAAACATAAGAAAGCCTGTGTGCATGGCGGG  
 AAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTCCGTGCCTTCGGCCCCCTTGCCCTG  
 CATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT  
 ACCCTTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTTGCCAGAGGACAAA  
 GCAGACCTTGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGCCCGGGTCT  
 CGTCCACACATCGGTATCCCCAAGCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGG  
 CCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAGATGAGGAACTGAGGCTCAG  
 AGAGGTGAAGTACCTGGCCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGA  
 AAGTCAGGAAGCAAGACTTCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCAC  
 GAAGGTCACTGGAACGTCTTCTAGCCACAGCCCTGGAGCTGAAGGTACGGCCAGTCCAGA  
 CAAAGTGACCAAGACATAACAAAGACCTTAACAGTTGCAGATATGAGCTGTATAATTGTGTT  
 ATTATATATTAATAAATAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 86**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902

><subunit 1 of 1, 451 aa, 1 stop

><MW: 49675, pI: 7.15, NX(S/T): 1

MVPEVRVLSSLLGLALLWFPLDSHARARPD MFCLFHGKRYSPGESWHPYLEPQGGLMYCLRCT  
CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKC VEPHTPSGLRAPPKSCQHNGTMYQHGEIF  
SAHELFP SRLPNQCVLCSTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEED  
SVQSLHGVRHPQDPCSSDAGRKRGP GTPAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKH  
KKACVHGGKTYSHGEVWHPAFRAFGLPCILCTCEDGRQDCQRVTCPT EYPCRHPKRVAGKC  
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKL V  
KDEETEAQRGEVPGPRPHSQNLPLDS DQESQEARLPERGTALPTARWP PRRSLERLPSPDFG  
AEGHGQSRQSDQDITKT

**Signal peptide:**

amino acids 1-25

**FIGURE 87**

CTAGCCTGCGCCAAGGGGTAGTGAGACGCGCGCAACAGCTTGCGGCTGCGGGGAGCTCCC  
 GTGGGCGCTCCGCTGGCTGTGCAGGCGGCC**ATGG**ATTCTTGCAGAAATGCTGATCTCAGT  
 CGCAATGCTGGGCGCAGGGGCTGGCGTGGGCTACGCGCTCCTCGTTATCGTGACCCCGGGAG  
 AGCGGCGGAAGCAGGAAATGCTAAAGGAGATGCCACTGCAGGACCCAAGGAGCAGGGAGGAG  
 GCGGCCAGGACCCAGCAGCTATTGCTGGCCACTCTGCAGGAGGCAGCGACCACGCAGGAGAA  
 CGTGGCCTGGAGGAAGAAGTGGATGGTTGGCGGCGAAGGCGGCGCCAGCGGGAGGTCACCGT**T**  
**G**AGACCGGACTTGCTCCGTGGGCGCGGACCTTGGCTTGGGCGCAGGAATCCGAGGCAGCC  
 TTTCTCCTTCGTGGGCCAGCGGAGAGTCCGGACCGAGATACCATGCCAGGACTCTCCGGGG  
 TCCTGTGAGCTGCCGTGGGTGAGCACGTTTCCCCAAACCTGGACTGACTGCTTTAAGGT  
 CCGCAAGGCGGGCCAGGGCCGAGACGCGAGTCGGATGTGGTGAAGTGAAGAAACCAATAAAA  
 TCATGTTCTCCAA  
 AAAAAAAAAA

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 60  
 50  
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 20  
 10  
 0

**FIGURE 88**

MDSL RKMLISVAM LGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLA  
TLQEAATTQENVAWRKNWMVGEGGASGRSP

**Signal peptide:**

amino acids 1-18



**FIGURE 89**

CAGGAGAGAAGGCACCGCCCCACCCCGCCTCCAAGACTAACCTCGGGCTTGAGGGGAAGAGGCTGACTGTACGTTCTCTTACTCTGGCACCCTCTCCAGGCTGCCATGGGGCCAGCACCCTCTCCTCATCTTGTTCTTTTGTATGTTGCGGACCCCTCCAAGGACAGCAGCACCACTTGTGGAGTACATGGAACGCCGACTAGCTGCTTTAGAGGAACGGCTGGCCAGTGCCAGGACCAGAGTAGTCGGCATGCTGCTGAGCTGCGGGACTTCAAGAAACAAGATGCTGCCACTGCTGGAGGTGGCAGAGAAGGAGCGGGAGGCACTCAGAACTGAGGCCGACACCATCTCCGGGAGAGTGGTCGCTCGGAGCGGGAGGTAGACTATCTGGAGACCCAGAACCAGCTCTGCCCTGTGTAGAGTTGATGAGAAGGTGACTGGAGGCCCTGGGACCAAGGCAAGGAAGAAGATGAGAAGTACGATATGGTGCACAGACTGTGGCTACACAATCTCAAGTGAGATCAATGAAGATTCTGAAGCGATTTGGTGGCCAGCTGTGCTATGGACCAAGGATCCACTGGGGCACAGAGAAGATCTACGTGTTAGATGGGACACAGAATGACACAGCCTTTGTCTTCCCAAGGCTGCGTGACTTCACCCTTGCCATGGCTGCCCGAAAGCTTCCCAGTGCCGGGTGCCCTTCCCCTGGGTAGGCACAGGGCAGCTGGTATATGGTGGCTTTCTTTATTTTGTCTGGAGGCCTCCTGGAAGACCTGGTGGAGGTGTGAGATGGAGAACACTTTCAGCTAATCAAATCCACCTGGCAAACCGAACAGTGGTGGACAGCTCAGTATTCCCAGCAGAGGGGCTGATCCCCCCTACGGCTTGACAGCAGACCTACATCGACCTGGTAGCTGATGAGGAAGGCTTTTGGGCTGTCTATGCCACCCGGGAGGATGACAGGCCTTGTGTCTGGCCAAGTTAGATCCACAGACACTGGACACAGAGCAGAGTGGGACACACCATGTCCCAGAGCAATGCTGAGGCTGCCTTTGTCTCTGTGGAGCCCTCTATGTGCTCTATAAACCCGCTGCTGCCAGTCGGGCCGACCTCAGTGCTCTTTTATGTCAGGCACCCCTGACCTCTGAACGGGCAGACGCTCCTTTATTTTCCCCGAGATATGGTGCCCATGCCAGCCTCCGCTATTAACCCCGAGAACGCCAGCTCTATGCGCTGGGATGATGGCTACCAGATTGTCTATAAGCTGGAGATGAGGAAGAAAGAGGAGGAGGTTTCAAGGAGCTAGCCTTGTTTTTGCATCTTTCTACTCCATACATTTATATTATATCCCCACTAAATTTCTTGTTCTCATCTTCAAATGTGGGCCATTGTGGCTCAAATCCTCTATATTTTTAGCCAATGGCAATCAAATCTTTTCTAGCTCCTTTGTTTCATACGGAACCTCAGATCCTGAGTAATCCTTTTAGAGCCCGAAGAGTCAAACCCCTCAATGTTCCCTCCTGCTCTCTTGGCCCATGTCAACAAATTTTCAAGCTAAGGATGCCCCAGACCCAGGCTCTAACCTTGATGCGGGCAGGCCAGGGAGCAGGCAGCAGTGTTCTTCCCCTCAGAGTGACTTTGGGAGGGAGAAAATAGGAGGAGACGTCCAGCTCTGTCTCTCTTCTCACTCCTCCTTCAGTGTCCTGAGGAACAGGACTTTCTCCACATTTGTTTTGTATTGCAACATTTTGCATTAAGAAAAGAAAATCCACAAAAAATAA

**FIGURE 90**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46038, pI: 6.50, NX(S/T): 2

MGPSTPLLILFLLSWGPLQGQHHLVEYMERRLAALEERLAQCQDQSSRHAAELRDFKNKM  
LPILLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR  
RNEKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL  
RDFTLAMAARKASRVRVFPFWVGTLVYGGFLYFARRPPGRPGGGEMENTLQLIKFHLAN  
RTVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCIAKLDPQTLDTQ  
QWDTPCPRENAEAAFFVICGTLVYVYNTRPASRARIQCSFDASGTLTPERAALPYFPFRYGAH  
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEV

**Important features:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 177-180, 248-251

**FIGURE 91**

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCGAG  
 AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTTCTCTCTAATCCAT  
 CCGTCACCTCTCCTGTCATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCC**atgg**  
 CTCTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT  
 GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGAGGACGCAGCATTCTCCTGTTTCTCTGTC  
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGGGTTCTTCAGGGGCCAGTTCTCTAGCGTGG  
 TCCACCTCTACAGGGACGGGAAGGACCAGCCATTATGCAGATGCCACAGTATCAAGGCAGG  
 ACAAACTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTGAGGCTGGAAAACATTAC  
 TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCTAGTCTTACTACCAGAAGGCCA  
 TCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCCTCTCATTTCCATCACGGGATATGTT  
 GATAGAGACATCCAGCTACTCTGTCACTCCTCGGGCTGGTTCCCCCGGCCACAGCGAAGTG  
 GAAAGGTCCACAAGGACAGGATTGTGCCACAGACTCCAGGACAAACAGAGACATGCATGGCC  
 TGTTTGATGTGGAGATCTCTTGACCGTCCAAGAGAACGCCGGGAGCATATCTGTTCCATG  
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTCGA  
 GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACCTGCTGTGGCCTATTTTGTG  
 GCATTGTTGGATGAAGATTTTCTTCTCAAATTCAGTGGAAAATCCAGGCGGAACGTGAC  
 TGGAGAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGAAACACGCAGTGGAGGTGAC  
 TCTGGATCCAGAGACGGCTACCCGAAGCTCTGCGTTTCTGATCTGAAAACGTAAACCCATA  
 GAAAAGCTCCCCAGGAGGTGCCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCT  
 TCTCAGAGTTTCCAAGCAGGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAAGGTG  
 GCGCGTGGGAGTGTGCCGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG  
 ATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTCACATTAAATCCCCGT  
 TTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCTGGACTATGAGTG  
 TGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCTGACATGTCGGT  
 TTGAAGGCTTATTGAGGCCTACATTGAGTATCCGTCTATAATGAGCAAAATGGAATCCC  
 ATAGTCATCTGCCAGTCAACCAGGAATCAGAGAAAGAGGCCTCTTGCAAAAGGCCTCTGC  
 AATCCAGAGACAAGCAACAGTGAGTCTCTCCTCACAGGCAACCAGCCCTTCTCCCCAGGG  
 GTGAAATG**Tag**GATGAATCACATCCACATTCTTCTTTAGGGATATTAAGGTCTCTCTCCCA  
 GATCCAAAGTCCCGCAGCAGCCGCCAAGGTGGCTTCAGATGAAGGGGACTGGCCTGTCC  
 ACATGGGAGTCAAGTGTCTATGGCTGCCCTGAGCTGGGAGGGAAGAAGGTGACATTACATTT  
 AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAGAACCG  
 TCAGGAATTCCTATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC  
 TTAGATCTTATTGATGACAGAGTGATCCTAATGGTTTGTTCATTATATTACACTTTCAGTA  
 AAAAAA

**FIGURE 92**

MALMLSLVLSLLKLGSGQWQVFGPKVPVQALVGEDAAAFSCFLSPKTNAEAMEVRFFRGQFSS  
 VVHLYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISSQSYQK  
 AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFFRPRTAKWKGFQGGDLSTDSTRNDRMH  
 GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF  
 FGIVGLKIFFSKFQWKIQAELDWRKHCQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVT  
 HRKAPQEVPHSEKRFTRKSVVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRKEYVTLS  
 PDHGYWVLRNLNGEHLTYFTLNPRFISVFPRTPTTKIGVFLDYECGTISFFNINDQSLIYTLTC  
 RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAIPESTSNESSSQATTPLP  
 RGE

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 239-255

**FIGURE 93**

GCGATGGTGC GCCCGGTGGCGGTGGCGGGCGGTTGCGGAGGCTTCCTTGGTCGGATTGCA  
 ACGAGGAGAAGATGACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGC  
 CATGAGGAGCCTGCCGAGCCTGGGCGGCCTCGCCCTGTTGTGCTCGCCGCCGCCGCCGCCGCG  
 CCGTCGCCCTCAGCCGCCTCGGCGGGGAATGTCACCGGTGGCGGGCGGGGCCGCCGGGCGAGGTG  
 GACGCGTTCGCCGGGCCCGGGGTTCGGGGGCGAGCCAGCCACCCCTTCCTTAGGGCGACGGC  
 TCCCACGGCCCCAGGCCCGAGGACCGGGGCCCGCGCGCCACCGTCCACCGACCCCTGGCTG  
 CGACTTCTCCAGCCCCAGTCCCGGAGACCAACCCCTCTTTGGGCGACTGCTGGACCCCTCTTCC  
 ACCACCTTTTCAGGCGCGCTCGGCCCTCGCCGACCACCCCTCCGGCGCGGGAACGCACCTTC  
 GACCACCTCTCAGGCGCCGACCAGACCCGCGCGGACCAACCCCTTCGACGACCACTGGCCCGG  
 CGCCGACCAACCCCTGTAGCGACCAACCGTACCGGCGCCACGACTCCCGGACCCGACCCCGC  
 GATCTCCCCAGAGCAGCAACAGCAGCGTCTCCCCACCCACCTGCCACCGAGGCCCCCTC  
 TTCGCTCCTCCAGAGTATGTATGTAACCTGCTCTGTGGTTGGAAGCCTGAATGTGAATCGCT  
 GCAACCAGACCAGGGCAGTGTGAGTGTGCGGCCAGGTTATCAGGGGCTTCAGTGTGAAACC  
 TGCAAGAGGGGCTTTTACCTAAATTACACTTCTGGGCTCTGTCAGCCATGTGACTGTAGTCC  
 ACATGGAGCTCTCAGCATACCGTGCAACAGGTTAA GCAACAGAGGGTGGAAGTGAAGTTTATT  
 TTATTTTAGCAAGGGAATAAAGGCTGCTACTCTCAAGGACCATACTGGTTTAAACAAAG  
 GAGGATGAGGGTCATAGATTTACAAAATATTTTATATACTTTTATTCTCTTACTTTATATGT  
 TATATTTAATGTGAGGATTTAAAAACATCTAATTTACTGATTAGTTCCTCAAAGCACTAG  
 AGTCGCCAATTTTTCTCTGGGATAATTTCTGTAATTTTCATGGGAAAAATTTATGAAGAA  
 AAATCTGCTTTCTGGAAGGGCTTTCAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTT  
 ATGTTTATTAATATACCATTGGAGTTTGAGGAAATTTGTTGTTGGTTTATTTTCTCTCTA  
 ATCAAAATCTACATTTGTTTCTTTGGACATCTAAAGCTTAACCTGGGGTACCCTAATTTA  
 TTTAAGTGTGTAAGTAGACTGGTTTACTCTATTTACCAGTACATTTTGTAGACCAAAAG  
 TAGATTAAGCAGGAATTATCTTTAAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGA  
 ATAATGTACTGTTATCTAAGCATTGCCTTGACTGCAGTGAAGTAATTTATCTTTGACCT  
 TATGTGAGGCACCTGGCTTTTGTGGACCCCAAGTCAAAAACTGAAGAGACAGTATTAAT  
 AATGAAAAAATAATGACAGGTTATACTCAGTGTAACTGGGTATAACCAAGATCTGCTGC  
 CACTTACGAGCTGTGTTCTTGGCAAGTAATTTCTTTCTACTGAGCTTGTTCCTTCTCAAG  
 GTTGTGTGAAGATTAATGAGTTGATATATATAAATGCCTAGCACATGTCACTCAATAAA  
 TCTGTTTGTGTTTAAATTTCAAAGGAATATTATGGACTGAATGAGAGAACATGTTTAAAG  
 ACTTTTAGCTCCTTGCAAGAAGTGCTTTATACTTTAGCACTAAATATTTTAAATGCTTTA  
 TAAATGATATTATACGTGTTATGGAATATTGTATCATATTGTAGTTTATTAATAATGTAGAAG  
 AGGCTGGGCGCGGTGGCTCACGCCCTGTAATCTAGCACTTTGGGAGGCCAAGCGGGTGGAT  
 CACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAACCCCGCTCTACTAAA  
 AATACAAACAAATAGCTGGGCGTGGTGGCACACACCTGTAGTCAGCTACTCCGGAGGCT  
 GAGGCGAGGAGATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGCGCCACT  
 GCATCCAGCCTGGTGAGAGAGGGAGACTCTGTCTTAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 94**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLPSILGGLALLCCAAAAA AVASAASAGNV TGGGGAAGQVDASPGFGLRGEPSHPFFPRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPETTP LWATAGPSSTTFQAPLGPSP TTPPAAERTS
TTSQAPTRPAPTTLSTTTGPAFTTPVATTVPAPTTPTPTDLPSSSNSSSVLPTPPATEAPS
SPPPEYVCNC SVVGLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLNYSGLCQPCDCSP
HGALSIPCNR
```

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

**EGF-like domain cysteine pattern signature.**

amino acids 214-226.

**FIGURE 95**

TGCGGCGCAGTGTAGACCTGGGAGG**ATG**GGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGG  
TCTCGGTGCCCCAGGGCCCAGGCCGTGTGTTGGGAAGACTGGACCCTGAGCAGCTTCTTGGG  
CCCTGGTACGTGCTTGCGGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAA  
GAACGTCGTGGGGGTGGTGGTGACCTCACTCCAGAAAACAACCTGCGGACGCTGTCTCTC  
AGCACGGGCTGGGAGGGTGTGACCAGAGTGTCATGGACCTGATAAAGCGAAACTCCGGATGG  
GTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGA  
CTATGCCATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGT  
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTACCAAGTGGAGCAGGAGC  
CTGGGCTTCCTGTCA**CAGTAG**CAGGCCCAGCTGCAGAAGGACCTACCTGTGCTCACAAAGAT  
CCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCCCTGTGACCTCGGCCA  
GTGTCCACCCACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCTCAGAATAAAGCGATTC  
CACAGCA

**FIGURE 96**

MGGLLLAAFLALVSVPRQAQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT  
LTPENNLRRTLSSQHGLGGCDQSVMDLIKRN SGWVFENPSIGVLELWVLATNFRDYAIIFTQL  
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

**Signal peptide:**

amino acids 1-20



**FIGURE 97**

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGACATGCTGCTGCTGCTGCTGCC  
 CCTGCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTT  
 CCGTGACGGTGACAGGAAGGCTGTGTGCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT  
 GGCTGGATTTACCCTGGCCAGTAGTTCATGGCTACTGGTTCGGGAAGGGCCAAATACAGA  
 CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC  
 GATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCTGAGCATCAGAGATGCCAGA  
 AGAAGTGATGCGGGGAGATACTTCTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA  
 ACATACCCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAG  
 GCACCTGGAGTCCGGCTGCCCCAGAAATCTGACCTGCTCTGTGCCCTGGGCCCTGTGAGCAG  
 GGGACACCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGAGCCCTCCACCAC  
 CCGCTCCTCGGTGCTCACCCTCATCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTCT  
 AGGTGACCTTCCCTGGGGCCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCCTAC  
 CCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG  
 AAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG  
 CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCCTGACCCTGTGCCCC  
 TCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCACCTGAGGGATGCAGCTGA  
 ATTCACCTGCAGAGCTCAGAACCCTCTCGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC  
 AGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTGGGGGAGCTGGAGCCACAGCCCTG  
 GTCTTCTCTGCTTCTGCGTCATCTTCGTTGTAGTGAGGTCTGCAGGAAGAAATCGGCAAG  
 GCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTCAGGGGTTCAGCCT  
 CTCAGGGGCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCAGCT  
 TCTGCCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCAGATGGT  
 GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC  
 ACAGATGAAGAAATGCAGAGACTCACCTGATTGAGGGATCAGAGCCCCCTCCAGGCAAGGGA  
 GAAGTCAGAGGCTGATTCTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACT  
 ATGAATTATGTGCAGAGTGAAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT  
 CCACACTGTGCCCTCCCTTTTATTTTTTAACATAAAGACAGACAATTCCTA

**FIGURE 98**

MLLLLLPLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFYSPSHGWIYPGPVVHGYWF  
 REGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKG  
 SIKWNYKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCVWPWACEQGTTPPMISWIGTSVS  
 PLDPSTTRSSVLTLPQPQDHGTSLTQVTFPGASVTNKTVHLNVSYPQNLTMTVFQGDG  
 TVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV  
 HLRDAAEFTCRAQNPLGSQQVYLNVSLSQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRS  
 CRKKSARPAAGVGDGTGIEDANAVRGASQGPLTEPWAEDSPDQPPPASARSSVGEGELQYA  
 SLSFQMVKPWDSEATDTEYSEIKIHR

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 351-370

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**FIGURE 99**

GACGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAG**ATGA**AGACCCTGTTCCCTG  
GGTGTACGCTCGGCCTGGCCGCTGCCCTGTCCCTTACCCTGGAGGAGGAGGATATCACAGG  
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGCCAGGA  
AGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTACCTTC  
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA  
ATACAGCGCCTATGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCAGGAGGGACCACT  
ACATCTTTTACTGCAAAGACCAGCACCATGGGGGCTGCTCCACATGGGAAAGCTTGTGGGT  
AGGAATTCTGATACCAACCGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGG  
ACTCTCGGAGGAGGACATTTTCAGCCCTGCAGACGGGAAGCTGCGTTCCCGAACAC**TAGG**  
CAGCCCCCGGCTGTCACCTCCAGAGCCACCCTACCACCAGACACAGAGCCCGGACCACCT  
GGACCTACCCTCCAGCCATGACCCTTCCCTGCTCCCACCCACCTGACTCCAAATAAAGTCCT  
TTTCCCCCAA

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**FIGURE 100**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404

<subunit 1 of 1, 170 aa, 1 stop

<MW: 19457, pI: 9.10, NX(S/T): 0

MKTLFLGVTLGLAAALSFTLEEEDITGTWYVKAMVVDKDFPEDRRPRKVSFVKVTALGGGKL  
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH  
MGKLVGRNSDTNREALLEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH

**Important features:****Signal peptide:**

amino acids 1-17

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**FIGURE 101**

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC  
 AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCC**ATG**AGGATTCTGCAGTTAA  
 TCCTGCTTGCTCTGGCAACAGGGCTTGTAGGGGAGAGACCAGGATCATCAAGGGGTTTCGAG  
 TGCAAGCCTCACTCCAGCCCTGGCAGGCAGCCCTGTTTCGAGAAGACGCGGCTACTCTGTGG  
 GCGGACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCACTGCCTCAAGCCCCGCTACA  
 TAGTTCACCTGGGGCAGCACACCTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC  
 ACTGAGTCCTTCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGA  
 CATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACC  
 TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCC  
 AGCCCCCAGTTACGCCTGCCTCACACCTTGCATGCGCCAACATCACCATCATTTGAGCACCA  
 GAAGTGTGAGAAGCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGG  
 AAGGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACCAGTCTTT  
 CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACAC  
 GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAAT**TAG**ACTGGACCCA  
 CCCACCACAGCCCATCACCTCCATTTCACCTTGGTGTGTTGGTTCCTGTTCACTCTGTAAAT  
 AAGAAACCTTAAGCCAAGACCTCTACGAACATTCTTGGGCCTCCTGGACTACAGGAGATG  
 CTGTCACTTAATAATCAACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATTCTGCCTT  
 GAAATATTGTGACTCTGGGAATGACAACACCTGGTTTGTCTCTGTTGTATCCCAGCCCCA  
 AAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTGCTAAATGAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 102**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27466, pI: 8.87, NX(S/T): 4

MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH  
 CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITW  
 AVRPLTLSSRCVTAGTSCLISGWGSTSSPQLRLPHTLRCANITIEHQKCNAYPGNITDTM  
 VCASVQEGGKDSQGDSCGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKN

**Important features:****Signal peptide:**

amino acids 1-18

**Serine proteases, trypsin family, histidine active site.**

amino acids 58-63

**N-glycosylation sites.**

amino acids 99-102, 165-168, 181-184, 210-213

**Glycosaminoglycan attachment site.**

amino acids 145-148

**Kringle domain proteins.**

amino acids 197-209, 47-64

**Serine proteases, trypsin family, histidine protein**

amino acids 199-209, 47-63, 220-243

**Apple domain proteins**

amino acids 222-249, 189-222

**FIGURE 103**

GAGCAGTGTCTGCTGGAGCCG**ATG**CCAAAAACCATGCATTTCTTATTCAGATTCATTGTTT  
TCTTTTATCTGTGGGGCCTTTTTACTGCTCAGAGACAAAAGAAAGAGAGACCCGAAGAA  
GTGAAAAAGAAAGTTTTCATCGTCCAGAAAACCTGCTCTAAGACAAGCAAGAAGGGAGACCT  
ACTAAATGCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCCTACTGCAGCCGGA  
CACAAATGAAGGCCACCCCAAATGGTTTGTCTTGGTGTGGGCAAGTCATAAAAGGCCTA  
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCTTCATT  
TGCATACGGAAAGGAAGGCTATGCAGAAGCAAGATTCCACCGGATGCTACATTGATTTTTG  
AGATTGAACTTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC  
ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA  
AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTTAGAAGATATTTTTAAGA  
AGAATGACCATGATGGTGATGGCTTCATTTCTCCCAAGGAATACAATGTATACCAACACGAT  
GAACTA**TAG**CATATTTGTATTTCTACTTTTTTTTTTTAGCTATTTACTGTACTTTATGTATA  
AAACAAAGTCACTTTTCTCCAAGTTGTATTTGCTATTTTCCCCTATGAGAAGATATTTGA  
TCTCCCAATACATTGATTTTGGTATAATAAATGTGAGGCTGTTTTGCAAACTTAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 104**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406

<subunit 1 of 1, 222 aa, 1 stop

<MW: 25794, pI: 6.24, NX(S/T): 1

MPKTMHFLFRFIVFFYLWGLFTAQRQKKEESTEEVKIEVLHRPENCSTSKKGDLLNAHYDG  
YLAKDGSKFYCSRTQNEGHPKWFEVLGVGQVIKGLDIAMTDMCPGEKRKVVIPPSFAYGKEGY  
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD  
KSYQDAVLEDFKKNDHGDGDFISPKEYNVYQHDEL

**Important features:****Endoplasmic reticulum targeting sequence.**

amino acids 219-222

**N-glycosylation site.**

amino acids 45-48

**FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 87-223, 129-142

**EF-hand calcium-binding domain proteins**

amino acids 202-214, 195-214



CAGAAA**ATG**CAGGGACATTGCTTCTTCCAGGCCCTGCTTTCTGCTGAGCCTCTTTGGAGCT  
GTGACTCAGAAAAACAAAACCTTCCTGTGCTAAGTGCCCCCAAATGCTTCTGTGTCAATAA  
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAAACATTACATTCC  
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTG**TAA**TCCCA GTTCTTTGGGAAG  
CCAAGGCAGGTGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATAGTGAAAC  
CCCGTGTCTACTAAAAATACAAAAATCAGCCGGGCGTGGTGGTGCATGCCTGCAATCCCAGT  
TACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCTCAGGAGGCAGAAGTTGCAGTGAACCC  
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA  
TAGTTTCTGTGTTTCATTTGCGGACTGCCCTCTCAGTGTTTCCTGGGATCCCCGCCAAATAA  
AGTACTTATATTCTC



**FIGURE 107**

CAAGCAGGTCATCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGGCAC  
 AGGGAAAGGGTGACCTCTGAGATTCCCCTTTTCCCCAGACTTTGGAAGTGACCCACC**ATGG**  
 GGCTCAGCATCTTTTTGCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT  
 TTC AATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGCAC  
 CAGCCTGCGCTGCGGGGGTGTCTTATTGACCACAGGTGGGTCTCACAGCGGCTCACTGCA  
 GCGGCAGCAGGTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCGAG  
 CAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGTACCTGGGAGCCTCGACGAGCCA  
 CGAGCAGACCTCCGGCTGCTGCGGCTGCGCCTGCCCGTCCGCGTAACCAGCAGCGTTCAAC  
 CCCTGCCCTGCCCAATGACTGTGCAACCGCTGGCACCAGAGTGCCACGCTCTCAGGCTGGGGC  
 ATCACC AACCACCCACGGAACCCATTCCCGGATCTGCTCCAGTGCCCTCAACCTCTCCATCGT  
 CTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATCACGAGCAACATGGTGTGTGCAG  
 GCGGCGTCCCGGGGCAGGATGCCTGCCAGGGTGATTCTGGGGGGCCCCCTGGTGTGTGGGGGA  
 GTCCTTCAAGGCTCTGGTGTCTGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG  
 AGTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAAC**TGAC**  
 CTGTTTCTCCACCTCCACCCCCACCCCTTAAC TTGGGTACCCCTCTGGCCCTCAGAGCACC  
 AATATCTCTCCATCACTTCCCCTAGCTCCACTCTTGTGGCCTGGGAAC TTCTTGGAAC TT  
 TAACTCCTGCCAGCCCTTCTAAGACCCACGAGCGGGGTGAGAGAAGTGTGCAATAGTCTGGA  
 ATAAATATAAATGAAGGAGGGGCAAAAAAAAAAAAAA

**FIGURE 108**

MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH  
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSV  
QPLPLPNDCATAGTECHVSGWGITNHPNPFDPDLLQCLNLSIVSHATCHGVYPGRITSNMVC  
AGGVPGQDACQGDSCGGPLVCGGVLQGLVSWGSGVPCGQDGI PGVYTYICKYVDWIRMIMRNN

**Signal peptide:**

amino acids 1-17

108/249

**FIGURE 109**

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC  
 CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCC**ATGT**CGGGCGAGCTCAGCA  
 ACAGGTTCCAAGGAGGAAGCGTTTCGGCTTGCTCAAAGCCCGGCAGGAGAGGAGGCTGGCC  
 GAGATCAACCGGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCCTCCAGAAAA  
 GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACCAATGAAGGCGAGATTGACC  
 TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCAAGACCCACCTGGAGATGAAG  
 AAGATGATCTCAGAGGTGACAGGAGGGGTGAGTACACTATATCCTACCGAGACTTTGTGAA  
 CATGATGCTGGGGAACGGTCGGCTGTCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA  
 ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCT**TGA**  
 GGACCCCGCTGGAATCCCCAGCCTTCCCACCCCATACCTCCCTCCCGATCTTGCTGCCCTT  
 CTTGACACACTGTGATCTCTCTCTCTCATTTGTTTGGTCATTGAGGGTTTGTGTTGTTT  
 TCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTGGGGAATCC  
 TGAGCCTTGGGTCCCCCTCTCTCTCTCTCCCTCCTTCCCGCTCCCTGTGCAGAAGGGCTG  
 ATATCAAACCAAAAACCTAGAGGGGGCAGGGCCAGGGCAGGAGGCTTCCAGCCTGTGTTCCC  
 CTTCACTTGGAGGAACAGCACTCTCCATCCTTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC  
 ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG  
 CTGCAGGGCCTCTTTCGGGTTTCCCTTGGACAGTGCCATGGTTCCAGTGCTCTGGTGTCACCC  
 AGGACACAGCCACTCTGGGGCCCCGCTGCCCCAGCTGATCCCACTCATTCACACCTCTTCT  
 CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTGGGAGCCCTTCAAGAAGG  
 TACCAGAAGGAACCTCCAGTCTGCTCTCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAG  
 CGTGCAGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAGTGAGGCTG  
 GGGTTTGGGGGAAAGGTGAGCTCAGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGGAC  
 CAGGATGGGAGAATGAGGAGTAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA  
 CTGAGAAATACAAGGTGCTGTGCTGACCCCAATCTGCTTGAAAAAAAAAAAAAAAAAAAA

**FIGURE 110**

MSGELSNRFQGGKAFGLLKARQERRLAEinREFLCDQKYSDEENLPEKLTAfKEKYMEFDLN  
NEGEIDLMSLKRMMEKLGVPKThLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVm  
MFEGKANESSPKPVGPPPERDIASLP

**FIGURE 111A**

CGCGCTCCCCGCGCGCTCCTCGGGCTCCACGCGTCTTGCCCCGAGAGGCAGCCTCCTCCA  
GGAGCGGGGCCCTGCAACACATGCCCCCGGGTGGGCAGGGGTGGCGCCGCCGCTGCGCGCC  
CGCCTGGCGCTGGCCTTGGCGCTGGCGAGCGTCTGAGTGGGCTCCAGCCGTCGCTTGCCC  
CACCAAGTGTACCTGCTCCGCTGCCAGCGTGGACTGCCACGGGTGGGCTCCGCGCGGTTC  
CTCGGGGATCCCCGCCAACGCTGAGCGCCTTGACCTGGACAGAAATATATCACCAGGATC  
ACCAAGATGGATCTTCGTGGGCTCAAGAACCTCCGAGTCTTGATCTGGAAGACAACCAAGT  
CAGCGTCACTGAGAGAGGCGCCTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCTGAACA  
AGAATAAGCTGCAAGTCTTCCAGAAATGCTTTTCCAGAGCACGCCGAAGCTCACCAGACTA  
GATTTGAGTGAACACAGATCCAGGGGATCCGAGGAAGGCGTTCCGCGGCATCACCAGTGT  
GAAGAACCTGCAACTGGACAACAACCATCAGCTGCATTGAAGATGGAGCCTTCCGAGCGC  
TGCGCGATTTGGAGATCCTTACCCTCAACAACAACAACATCAGTCGCATCCTGTACCAGC  
TTCAACCACATGCCGAAGATCCGAACCTGCGGCCTCCACTCCAACCACCTCTACTGCGACTG  
CCACTTGGCCTGGCTCTCGGATTTGGCTGCGACAGCGACGGACAGTTGGCCAGTTTCACTCT  
CAGCTGGCTCCTGTGCATTGAGGGGCTTCAACGTGGCGGATGTGCAGAAGAAGGAGTACGTG  
TGCCAGCCCCCACTCGGAGCCCCCATCTGCAATGCCAACTCCATCTCCTGCCCTTGGCC  
CTGCACTGCGAGCAATAACATCTGTGGACTGTGAGGAAAAGGGCTTGATGGAGATTCCTGCCA  
ACTTGGCGGAGGCGATCGTCGAAATACGCTTGAACAGAACTCCATCAAAGCCATCCTTGCA  
GGAGCCTTACCAGTACAAGAACTGAAGCGAATAGACATCAGCAAGATCAGATATCGGA  
TATTGCTCCAGATGCTTCCAGGGCGTAAATCACTACATCGTGGTCTGTATGGGAACA  
AGATCCAGGAGATTGCCAAAGGAGCTGTTTGTATGGGCTGGTGTCCCTACAGCTGCTCCTCCTC  
AATGCCAACAGATCACTGCTGCGGGTGAACACGTTTCAGGACCTGCAGAACCTCAACTT  
GCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTTCCGCCCTCTGCAAT  
CCATCCAGACACTCCACTTAGCCCAAACCCATTTGTGTGCGACTGCCACTTGAAGTGGCTG  
GCCGACTACTCCAGGACAACCCCATCGAGACAAGCGGGGCCGCTGCAGCAGCCCGCGCG  
ACTCGCCAAACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCCGCTGCTCAGGCTCCGAGG  
ATTACCGCAGCAGGTTTCAAGCAGCGAGTGTTCATGGACCTCGTGTGCCCCGAGAAGTGTCCG  
TGTGAGGGCAGCAGTTGTGGACTGCTTCAACCAAGAAGCTGGTCCGATCCCAAGCCACTCC  
TGAATATGTACCGGACCTGCGACTGAATGACAAATGAGGTATCTGTTCTGGAGGCCACTGGCA  
TCTTCAAGAAGTTGCCAACCTGCGGAAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG  
CGAGAGGGAGCTTTTCGATGGAGCAGCAGCGCTGCAGGAGCTGATGCTGCAGGGAACCAAGCT  
GGAGACCGTGCACGGGCGCGTGTCCGTGGCCTCAGTGGCCTCAAACCTTGTATGCTGAGGA  
GTAACCTTGATCAGCTGTGTGAGTAATGACACCTTTTCCGCCCTGAGTTCCGTGAGACTGCTG  
TTAECTCATATGACATCCGATCACCACCATCACCCTGGGGCTTACCACGCTTGTCTCCCT  
GTCCACCATAAACCTCTGTCCAACCCCTTAACTGCAACTGCCACCTGGCCTGGCTCGGCA  
AGTGTTGAGGAAGAGGCGGATCGTCAAGTGGGAACCTAGGTGCCAGAAGCCATTTTCTCCT  
AAGGAGATTCCCATCCAGGATGTGGCCATCCAGGACTTCACTGTGATGGCAACGAGGAGAG  
TAGCTGCCAGCTGAGCCGCGCTGCCCGGAGCAGTGCACCTGTATGGAGACAGTGGTGGCAT  
CGAGCAACAAGGGGCTCCGCGCCCTCCCAAGGCAATGCCAAGGATGTGACCGAGCTGTAC  
CTGGAAGGAACCACTTAAAGCCGTGCCAGAGAGCTGTCCGCCCTCCGACACCTGACGCT  
TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAATACATGTCTC  
ACCTCTCCACTCTGATCTGTAGCTACAACCGGCTGAGGTGCATCCCCGTCCACGCTTCAAC  
GGGCTGCGGTTCCTGCGAGTGCTAACCCTCCATGGCAATGACATTTCCAGCGTTTCTCGAAG  
CTCTTCAACGACCTCACATCTCTTTCCATCTGGCGCTGGGAACCAACCCACTGCTGAGT  
ACTGCAGTCTTCGGTGGCTGTCGGAGTGGGTGAAGGCGGGGTACAAGGACCTGGCATGCTC  
CGCTGCGATGAGCCTGAGCCATGGCTGACAGGCTCCTGTCAACCCCAACCCACCGCTT  
CCAGTCAAAGGGCGGATGGACATCAACATTTGTGGCAATGCAATGCTTGCCTTCCAGCC  
CGTGCAAGAATAACGGGACATGCACCCAGGACCTGTGAGAGCTGTACCGCTGTGCTGCCCC

**FIGURE 111B**

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCA  
 GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTTCAGCTGCTCCTGCCCTC  
 TGGGCTTTGAGGGGCAGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAA  
 AACAAATGCCACCTGCGTGGACGGGATCAACAACACGTGTGTATCTGTCCGCCTAACTACAC  
 AGGTGAGCTATGCGACGAGGTGATTGACCACCTGTGTGCTGAGCTGAACCTCTGTGAGCATG  
 AGGCCAAGTGCACTCCCCCTGGACAAAGGATTGAGCTGCGAGTGTGTCCCTGGCTACAGCGGG  
 AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCACAAGTGCCGCCACGGGGCCAGTG  
 CGTGGACACAATCAATGGCTACACATGCACTGCCCTGCCCCAGGGCTTCAGTGGACCTTCTGTG  
 AACACCCCCCACCCTGGTCCTACTGACAGACCAGCCATGCGACCAGTACGAGTGCCAGAAC  
 GGGGCCCAGTGATCGTGGTGAGCAGGAGCCCACTGCCGTGCCACACAGGCTTCGCCGG  
 CCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAGACTCCTACGTGGAACCTGG  
 CCTCCGCCAAGGTCCGACCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAGGACAAC  
 GGCATCCTTCTCTACAAAGGAGACAATGACCCCTGGCACTGGAGCTGTACCAGGGGCCAGT  
 GCGGCTGGTCTATGACAGCCTGAGTTCCTCCCAACCACAGTGTACAGTGTGGAGACAGTGA  
 ATGATGGGCAGTTTCACAGTGTGGAGCTGGTGACGCTAAACCAGACCCCTGAACCTAGTAGTG  
 GACAAAGGAACTCCAAAGAGCCTGGGGAAGCTCCAGAAGCAGCCAGCAGTGGGCATCAACAG  
 CCCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCTCTCCGCTTGGCCAGGGCAGCG  
 ACCGGCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCAG  
 GACTTCAAGGCCCTCCACCACAGTCCCTGGGGGTGTCAACAGGCTGCAAGTCTGTACCCGT  
 GTGCAAGCACGGCTGTGCCGTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAG  
 GCTGGACCGGCCACTCTGCGACCAAGGAGGCCCGGGACCCCTGCCCTGGGCCACAGATGCCAC  
 CATGGAAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCCGAGGGCTATGGAGG  
 GGACTTGTGTGACAACAAGAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTGACCATG  
 GGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCTGTGCCAGCCCGGCTTACGGGC  
 GAGCACTGCCAACAAGAGAATCCGTGCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCA  
 GAAAGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCCATCATGGAATGTCTGGGGGCT  
 GTGGCCCCAGTGTGTGCCAGCCACCCGACGCAAGCGCGGAAATACGTCTTCCAGTGACAG  
 GACGGCTCCTCGTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGGCGCTGCCTGCGGTGTTT  
 CTAAGCCCCTGCCCGCCTGCCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCC  
 ATGTGGGACCCCTGGTGATTACGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAGGAAGA  
 AGAGAATATTAAGTATATTGTAAATAAACAAAAAATAGAACTTAAAAA



**FIGURE 112**

MAPGWAGVGA AVRARLALALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRN  
 AERLDLDRNNITRITKMFAGLKNLRLVHLEDNQVSVIERGAFQDLKQLERLRNLKNKLQVL  
 PELLFQSTPKLTRLDSLSENIQIGIPRKAFRGITDVKNLQLDNNHISCIEDGAFRALRDLIEL  
 TLNNNNISRLVTSFNHMPKIRTLRLHSNHLYCDCHLAWLSDWLQRRTVGQFTLCMAPVHL  
 RGFNVADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV  
 EIRLEQNSIKAIPAGAFQYKKLKRIDISKNQISDIAPDAFQGLKSLTSLVLYGNKITEIAK  
 GLFDGLVSLQLLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQTIISKGLFAPLQSIQTLHL  
 AQNPFCVDCHLKWLADYLQDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDYRSRFS  
 SECFMDLVCEPKCRCEGTIVDCSNQKLVRIPSHLPEYVTDLRLNDNEVSVLEATGIFKKLPN  
 LRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTLMLRSNLISCV  
 SNDTFAGLSSVRLLSLYDNRIITITPGAFTTLVSLSTINLLSNPFNCNCHLAWLGKWLKRKR  
 IVSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRCSNKGLR  
 ALPRGMPKDVTELYEGNHLTAVPRELSALRHLLIDLSNNSISMLTNYTFSNMHLSTLIL  
 SYNRLRCIPVHAFNGLRSLRVLTLHGNDISSVPEGSFNDLTSLSHLALGTNPLHCDCLRWL  
 SEWVKAGYKEPGIARCSSPEPMADRLLLTTPTHRFQCKGPVDINIVAKCNACLSSPCKNNGT  
 CTQDPVELYRCACPYSYKGDCTVPINTCIQNPCQHGGTCHLSDSHKGDFSCSCPLGFEGQR  
 CEINPDCCEDNDCENNATCVDGINNYVICPPNYTGELCDEVIDHCVPELNLQHEAKCIPL  
 DKGFSCECVPGYSGLKCETDNDDCAHKKRGAQCVDITNGYTCCTCPQGFSGPFCEHPPPMV  
 LLQTSPCDQYECQNGAQCIVVQQEPTCRCPPGFAGPRCEKLITVNFVGKDSYVELASAKVRP  
 QANISLQVATDKDNGILLYKGDNDPLALELYQGHVRLVYDSLSPPTTVYSVETVNDGQFHS  
 VELVTNLQTLNLVVDKGTPKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF  
 HGCIEHVRINNELQDFKALPPQSLGVSFGCKSCTVCKHGLCRSVEKDSVVCECRPGWTGPLC  
 DQEARDPCLGHRCHHGKCVATGTSYMCKCAEGYGGDLCDKNKDSANACSAFKCHHGQCHISD  
 QGEPYCLCQPGFSGEHCQQENPCLGQVVREVIRRQKGYASCATASKVPIMECRGGCGPQCCQ  
 PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

**Signal peptide:**

amino acids 1-27

**FIGURE 113**

GGATGCAGGACGCTCCCTGAGCTGCCTGTCCCGACTAGGTGGAGCAGTGTTCCTCCGCA  
GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCT  
CCGGCAGGCTTTGAGGATGAAGGCTGCGGGCATTCTGACCCTCATTTGGCTGCCTGGTCACAG  
GCGCCGAGTCCAAATCTACACTCGTTGCAAACCTGGCAAAATATTTCTCGAGGGCTGCGCTG  
GACAATTACTGGGGCTTCAGCCTTGAAACTGGATCTGCATGGCATATTATGAGAGCGGCTA  
CAACACCACAGCCCCGACGGTCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA  
ACAGCTTCGCGTGGTGCAGACGCGAAAGCTGAAGGAGAACAACCACTGCCATGTGCGCTGC  
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA  
GACACAAGGAATGAACTATTGGCAAGGCTGGAAGAAAACATTGTGAGGGCAGAGACCTGTCCG  
AGTGGAAAAAAGGCTGTGAGGTTTCTTAACTGGAACCTGGACCCAGGATGCTTTGCAGCAAC  
GCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTCATCTTGTCCTGTTTCCCTCCCAATA  
TTCCTTCTCAAACCTGGAGAGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTTCCAT  
TTAAATGTC

**FIGURE 114**

MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP  
 TVLDDGSIDYGIFQINSFAWCRRGKLKENNHCHVACSALITDDLTDALICARKIVKETQGMN  
 YWQGWKKHCEGRDLSEWKKGCEVS

**Signal peptide:**

amino acids 1-19

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**FIGURE 115**

CAGGCCATTGTCATCCCACTGTCCTTGTGTTTCGGAGCCAGGCCACACCGTCCTCAGCAGTGT  
 CATGTGTTAAAAACGCCAAGCTGAATATATC**ATG**CCCCCTATTAAAACTGTACATGGCTCCC  
 CATTGGTTTTTGGAGAAAAGTTCAAGCTTTTTACCTTGGTGTCTGCCTGTATCCCAGTGTTT  
 AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGTCACTTCCCAGATCTGCTTCTCAC  
 CAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA  
 CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTAAGGAA  
 ACATTCAAGTCCCTGTCTCACATAGACCCGTATGTCCTCTATCCATCTCTAAATGTACCAG  
 CTTTGACTCAGTTGTTCTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGC  
 TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA  
 CAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTTCATCTGATCGTGGCAGGTGG  
 TTATGACGAGAGAGTCTCGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAA  
 AGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTCTCAGACAAACAGAAAATCTCC  
 CTCTCCACAGCTGCAGTGTGTGCTTTACACACCAAGCAATGAGCATTGGCATTGTCCC  
 TCTGGAAGCCATGTACATGCAGTGCCAGTCATTGCTGTTAATTCGGGTGGACCCCTTGAGT  
 CCATTGACCACAGTGTACAGGGTTTCTGTGTGAGCCTGACCCGGTGCATTCTCAGAAGCA  
 ATAGAAAAGTTCATCCGTGAACCTTCCTTAAAGCCACCATTGGGCTGGCTGGAAGAGCCAG  
 AGTGAAGGAAAAATTTCCCTGAAGCATTTACAGAACAGCTCTACCGATATGTTACCAAAC  
 TGCTGGTAT**TAA**TCAGATTGTTTTTAAGATCTCCATTAAATGTCATTTTTATGGATTGTAGACC  
 CAGTTTTGAAACCAAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTAAAAAATAAA  
 CTTGAGTCTTGAATGTGAGCCACTTTCCTATATACCACACCTCCCTGTCCACTTTTCAGAAA  
 AACCATGTCTTTTATGCTATAATCATTCCAAATTTTGCCAGTGTTAAGTTACAAATGTGGT  
 TCATTCCATGTTTCAGCAGAGTATTTTAATTATATTTCTCGGGATTATTGCTCTCTGTCTA  
 TAAATTTTGAATGATACTGTGCCTTAATTGGTTTTTCATAGTTTAAAGTGTGTATCATTACAA  
 AGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCACAGATTCAAT  
 CCACCGAAGTGTTCACTGTCATCTGTTAGGGAATTTTGTGTTGCTGTCTTGCCTGGATC  
 CATAGCGAGAGTGCTCTGATTTTTTTTAAGATAATTTGTATTTTTGCACACTGAGATATAA  
 TAAAGGTGTTTATCATAAAAAATAAAAAAAAAA

**FIGURE 116**

MPLLKL VHGSPLVFG EKFKLFTLVSACIPVFLRARRRKKILFYCHFPDLLLTKRDSFLKRLY  
 RAPIDWIEEYTTGMADCILVNSQFTA AVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLD  
 DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGR LTSQDWERVHLIVAGGYDERVLENVE  
 HYQELKKMVQQSDLGQYVTF LRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCFV  
 IAVNSGGPLESIDHSVTGFLCEPDVHFSEAI EKFI REPSLKATMGLAGRARVKEKFSPEAF  
 TEQLYRYVTKLLV

**Signal peptide:**

amino acids 1-15

1-15  
 16-30  
 31-45  
 46-60  
 61-75  
 76-90  
 91-105  
 106-120  
 121-135  
 136-150  
 151-165  
 166-180  
 181-195  
 196-210  
 211-225  
 226-240  
 241-255  
 256-270  
 271-285  
 286-300

**FIGURE 117**

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACCATGTTGGACTTCGCGATCTT  
 CGCCGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGAC  
 AAGCTGCAGGAATTCCAGGGATTACTCCAACGAAGAAAAAGATGGTAATCTTCCAGATATT  
 GTGAATAGTGGAAGTTTGCATGAGTTCCTGGTTAATTTGCATGAGAGATATGGGCCGTGGT  
 CTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTACTGAAGCAGC  
 ATATCAATCCCAATAAGACATCGGACCCTTTTGAACCATGCTGAAGTCATTATTAAGGTAT  
 CAATCTGGTGGTGGCAGTGTGAGTGAAAACCATGAGGAAAAAATTGTATGAAAATGGTGT  
 GACTGATTCTCTGAAGAGTAACTTTGCCCTCCTCTAAAGCTTTCAGAAGAATTATTAGATA  
 AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTTGGTTTTGCT  
 ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTG  
 CTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAGGCTTTCTAGATGGGTAC  
 TTGATAAAAAACATGACTCGGAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT  
 TTAAGGAACATCATAAAGAACGAAAGGAAGGAACCTCAGTCAACATATTTTCATTGACTC  
 CTTAGTACAAGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG  
 CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGGCAATCTGTTTTTAAACCACCTCTGAA  
 GAAGTTCAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGGAAATGGTCTGTACTCC  
 AGAGAAAATTGAGCAGCTCAGATATTGTGAGCATGTGCTTTGTGAACTGTTGAACTGCCA  
 AACTGACTCCAGTTTCTGCCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTATTATT  
 CCTAGAGAGACCCCTCGTCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCC  
 ATCTCCACACAAGTTTGTATCCAGATCGGTTTGTATGATGAATTAGTAATGAAAACTTTTCTCT  
 CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTTGATATATGGTGACCACA  
 GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTCTGTGGAGGGACAGGTTATTGA  
 AACAAAGTATGAACFGTTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT  
 ATTAAAATTTTATACATTAAAAATCATTGTTAAATTGATTGAGGAAAAACAACCATTTAAAAA  
 AAATCTATGTTGAATCCTTTTATAAACCAAGTATCACTTTGTAATATAAACACCTATTGTGAC  
 TTAA

**FIGURE 118**

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH  
ERYGPVVSFWFGRRLLVSLGTVDLVKQHINPNKTSDPFETMLKSLRLRYQSGGGSVSENHMRK  
KLYENGVTDSLKSNFALLLLKSEELLDKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE  
DDQEVIRFQKNHGTWVSEIGKGFLDGSGLDKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS  
QHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTWAICFLTTSSEEVQKKLYEEINQVF  
GNGPVTPEKIEQLRYCQHVLCEVVRTAKLTPVSAQLQDIEGKIDRFIIIPRETLVLVYALGVVL  
QDPNTWPSPHKFDPDRFDDELVMKTFSSSLGFSGTQCEPELRFAYMVTTVLLSVLVKRLHLLS  
VEGQVIETKYELVTSSREEAWITVSKRY

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 271-290

**FIGURE 119**

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGA  
 GACCGCCGCCCTTGTCCTCCGAGGGGCC**AT**GGGCCGGGTCTCAGGGCTTGTCCTCTCGCTTC  
 CTGACGCTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACAT  
 ACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTCAGCTGG  
 TGGCCGCGCTCTCTGTACCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCTCTCAGGA  
 GTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT  
 GGCCCTGTCTTCTTCATATTCGAGCGTTGGGAGTGCACGTATTGGTACATTTTTGTCT  
 TCTGCAGTGCCCTTCCAGCTGTCACTGAAATGGCTTTATTTCGTCACCGTCTTTGGGCTGAAA  
 AAGAAACCCTTCT**TGA**TTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG  
 CCGCTTCGTATTCTTGAAGAAGGAAGGCATAGGCTTCGGTTTTCCCTCGGAAACTGCTTC  
 TGCTGGAGGATATGTGTTGGAATAATTACGCTTTGAGTCTGGGATTATCCGCATTGTATTTA  
 GTGCTTTGTAATAAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTTAGGGGACA  
 ATTA



Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

TCCCGGACCCCTGCCGCCCTGCCACT**ATG**TCCCGCCGCTCTATGCTGCTTGCCCTGGGCTCTCC  
CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCTGCTGCAGCCCCATA  
GTGCCCGGAACGAGTGAAGGCCCTGGCATCAGAGTGCGCCACGACCTTGAGCCTGCCCTT  
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCCGCTCGTGCCAGC  
AGCAGGCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCCAGCTGGGCTAC  
AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAACCTTACCGGTGC  
CCACTCAGGTCACTTATGGAACCCCATGTCCATTGGCATCAGCTTCATGGGCAACTACATGG  
ATCGGGTGCCACACCCAGGCCATCCGGGCAGCCAGGGCTACTGGCCTCGGTTGTGGCT  
CAGGGAGCCCTGAGGTCCAACATATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC  
TCCAGGCAACCACTCTACCACCTCATCCAGAATTGGCCACATACCGCTCCCCCT**TGA**GGCC  
CTGCTGATCCGCACCCCATTCCTCCCCCTCCCATGGCCAAAAACCCCACTGTCTCCTTCTCCA  
ATAAAGATGTAGCTC

**FIGURE 122**

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT  
AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP  
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL  
IQNWPHYRSP

**Signal peptide:**

amino acids 1-20

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**FIGURE 123**

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAG**ATG**CAACT  
 GACTCGCTGCTGCTTTCGTGTTCTTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG  
 ATGATGGTCTCCCGGCTCAGAGGACCCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCCC  
 CGGGTGCCTCGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCT  
 CCTAGGGTGCTGGCCCCGCCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCC  
 CGAACCCAGCCCCCACCCCTCAGCCAAGGTGAAGAAATCTTTGGCTGGGGCGACTTCTAC  
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAA  
 TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC  
 TCGTCCCCCCAGTAAAGCTGTAGAGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAG  
 GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCGCCGGACCTC  
 GCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCAGCCACCT  
 GGAGCTGCTCCCAGCCCTTCAAAGTCTGTCTGTGTCTACATCGCCTTCTACAGCACGGACTAT  
 CGGCTGGTCCAGAAGGTGTGCCAGATTACAACATACCATAGTGATACCCCTACTACCCATC  
 TGGG**TGA**CCCCGGGGCAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCATGC  
 AGGAGACCATCTGGACACCGGGCAGGGAAGGGGTTGGGCCTCAGGCAGGAGGGGGGTGGAG  
 ACGAGGAGATGCCAAGTGGGGCCAGGCCAAGTCTCAAGTGGCAGAGAAAGGTTCCCAAGTG  
 CTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTGGGCT  
 CTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC  
 TGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTT  
 CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACAGCCTG  
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCTTAGGAGCCAGTCAGCAGGGTGGGGTGGGGC  
 CAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCTTGTCTGTGCTGAGCATG  
 GCATGAGGCTGAAGTGGCAACCCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTC  
 CAGCCAGGCCACCCCTTTCAAAATTCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATT  
 GCTGATGGCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCCACTAAGGCC  
 ACAGCCCATCCGCGTGCTGTGTGTCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAG  
 CATCCATGTCCCGGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTGACAGCGGGGTCTCC  
 CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCCGGCCGAGA  
 GCATGTGCTGGATCTGTTCTGTGTGCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTGT  
 GAAACCGTGATTGCTGACTTTTGTGTGAAGAATCGTGTTCTTGAGCAGGAAATAAAGCTT  
 GCCCCGGGGCA

**FIGURE 124**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521  
><subunit 1 of 1, 252 aa, 1 stop  
><MW: 28127, pI: 8.91, NX(S/T): 5  
MQLTRCCFVFLVQGSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN  
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD  
HNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGR  
RTSLCTHDPKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVCPCDYNHSDTPY  
YPSG

**Important features of the protein:****Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71

**FIGURE 125**

GTGAATGTGAGGGTTTGATGACTTTCAGATGTCTAGGAACCAAGTGGGTGCAGGGGCCCCA  
 GGCAGGGCTGATTCTTGGGCGGAGGAGAGTAGGGTAAGGGTTCTGCATGAGCTCCTTAAAG  
 GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT  
 TGGTGAAGTGTGCGCGCCGCCGCCGCTCGCTCCTGCAGCGCTGTCGACCTAGCCGCTAG  
 CATCTTCCCAGCACC GGATCCCGGGTAGGAGGCGACGCGGGCGAGCACCAGCGCCAGCC  
 GGCTGCGGCTGCCACACGGCTCACCATGGGGCTCCGGGCGCGGGCGCTGTCCGCGGTGCCG  
 GCCGTGCTGCTGGTCTCACGCTGCCGGGGCTGCCCGTCTGGGCACAGAACGACACGGAGCC  
 CATCGTGTGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGGCCACGGACTCCAAGG  
 GCTCTCTTCTCCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGGTCGCTTCTCG  
 GCGGTGCGGAGCACCACACAGCCATCCGAGATGAGCAACAAGACGCGCATCATTTACTT  
 CGATCAGATCCTGGTGAATGTGGTAATTTTTTTCACATTGGAGTCTGTCTTTGTAGCACC  
 GAAAAGGAATTTACAGTTTCAGTTTTTTCACGTGATTAAAGTCTACAGAGCCAACTATCCAG  
 GTTAACTTGATGTTAAATGGAACACAGTAATATCTGCCTTTGCGGGGGACAAAGATGTTAC  
 TCGTGAAGCTGCCACGAATGGTGTCTGCTCTACCTAGATAAAGAGGATAAGGTTTACCTAA  
 AACTGGAGAAAGGTAATTTGGTTGGAGGCTGGCAGTATTCCACGTTTTCTGGCTTTCTGCTG  
 TCCCCCTATTAGGATTCAATTTCTCCATGATGTTTCATCCAGTGAGGGATGACCCACTCCTG  
 AGTTATTTGAAGATCATTTTTTTCATCATTGGATTGATGTCTTTTATTGGTTTCTCATGGGTG  
 GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTTTCAGATTATTTGTG  
 TGTGTCTGTTTCAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA  
 ACAGTCAAAGCTGTCTGCAAGACTTATTCTGAATTTTCTTCTGGGATTACTGAATTAGT  
 TACAGATGTGGAATTTTATTTGTTTAGTTTTTAAAGACTGGCAACCAGGTCTAAGGATTAGA  
 AAACCTCTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG  
 TGTTAATATATTGATTATATTTGTTTTTATCTCCTTTGGAATTAGTTTGTTTGGTTCTTGTA  
 AAACTTGGAATTTTTTTTTTTCAGTAACTGGTATTATGTTTTCTCTTAAAAATAAGGTAATGAA  
 TGGCTTGCCACAAATTTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAAAA  
 GAATGCTTCATAGTTGTATTTTAATTGTATATGTGAAGAGTCATATTTTCCAAGTTATAT  
 TTCTAAGAAGAAGATAGATCATAAATCTGACAAGGAAAAAGTTGCTTACCCAAAATCTAAG  
 TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCTCCGAGGGAAATCTTATACTTTATTGC  
 TCAACTTTAATTTAAATGATTGATAATAACCACCTTTATTTAAAAACCTAAGGTTTTTTTTTT  
 TCCGTAGACATGACCACTTTATTAACTGGTGGTGGGATGCTGTTGTTTCTAATTATACCTAT  
 TTTTCAAGGCTTCTGTTGATTTGAAGTATCATCTGTTTTGCTTAACTCTTTAAATTTGTA  
 TATATTTATCTGTTTAGCTAATATTTAAATTCAAATATCCATATCTAAATTTAGTGCAATAT  
 CTTGTCTTTGTATAGGTCATATGAATTCATAAAATTATTTATGTCTGTTATAGAATAAAGA  
 TTAATATATGTTAAAAAA

**FIGURE 126**

MSGRRALSAVPAVLLVLTLPGLPVWAQNDEPIVLEGGKCLVVCDSNPATDSKGSSSSPLGI  
SVRAANSKVAFSAVRSTNHEPSEMSNKTRIIFYDQILVNVGNFFTLESV FVAPRKG IYSFSF  
HVIKVYQSQTIQVNLMLNGKPVISAFAGDKDVTREAA TNGVLLYLDKEDKVYLKLEKGNLVG  
GWQYSTFSGFLVFPL

**Signal peptide:**

amino acids 1-27

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**FIGURE 127**

CGGTGGCC**ATG**ACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTC  
GCCCTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGC  
TTTCTTCTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTA  
TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTC  
TATATCCAAGAAATGTTCCGATTGTCATATTATAAACTCTTAAAAAAGCCAGTGAAGTTT  
GAAGAGTATAAACCCAGGTGAGACAGCACCTCTATGCGACTGCTGGCCTATGTTTCTGGCT  
TGGGCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCATCTGACTCCTTGGG  
CCAGGCACAGTGGGCATTTCATGGAGATTCCTCAATTCTTCCTTTATTGAGCTTTCATGAC  
GCTGGTCATTATCTTGCTGCATGTATTCCTGGGCATTGTATTTTTTGATGGCTGTGAGAAGA  
AAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTGAGCCAGACCTTC  
ATAAGTTCCTATTATGGAATAAACCTGGCGTCAGCATTATAATCCTGGTGTCTATGGGCAC  
CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG  
ACAAGAACTTTCTCTTTACAACAGCGCTCCAGAT**TAA**CCTCAGGGAACAGCACTTCCCAA  
ACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCTTTTTCTGAAAATCCCTTTTCTG  
GTGGAATTGAGAAAGAAATAAACTATGCAGATA

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**FIGURE 128**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN
KDGPQTQYLLIFGAFVSYYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLAYVSGLGF
GIMSGVFSFVNTLSDSLGPCTVGIHGDSPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKW
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLKLCLLCQDKN
FLLYNQSR
```

**Important features of the protein:****Signal peptide:**

amino acids 1-19

**Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

**Glycosaminoglycan attachment site.**

amino acids 120-123

**Sodium:neurotransmitter symporter family protein**

amino acids 31-65

**FIGURE 129**

CGGCACACGACGCGCCACACCGCTGCCACTGCCGCCCTGCCGGGGCC~~ATG~~TCGCTCTGGGCTTGCCCTTCT  
 TGGTGCTCTTGGTGGCCTCGGTGCGAGAGCCATCTGGGGGTTCTGGGGCCCCAAGCAAGCTCTGCGAGAAAGACGCCG  
 AGTTTGAAGCGGCTACGTGGACAGAGGTCAACAGCGAGCTGGTCAACATCTACACATCTCAACCATCTGTGACCC  
 GCAACAGGACAGAGGCGTGCCTGTGTCTGTGAACCTCTGAACAGCAGAGAGGGGGCGCGCTGTGCTGTTTGTGG  
 TCCGCGAGAGGAGGCTGTGGTGTCTTCCAGGTGCCCTAATCTGCGAGGAGTGTTCACGCGCAAGTAACTCT  
 ACCAAAAAGTGAACGAACCTGTGTGAGCCCCCAACCAAGAATGAGTCGGAGATTCAGTTCTTCTACGTGGATG  
 TGTCCACCTGTGCACAGTCAACACACATACAGCTCCGGGTACGCCGATGGACGATTTTGTGCTCAGGACTG  
 GGGAGCAGTTGAGTCTCAATACCAAGCAGCAGCAGCCCGAGTACTCAAGTATGAGTTCCTGAGGCGGTGGACT  
 CGGTAAATTTGACAGTCAAGTCCCAACAGGCTTCCCTGCTCAGTCTCAGTATCAGGATGTCTGTGTGCTGCT  
 TCTATGACCTGGACAACAGTAGCCTTTCATGGCATGTACAGACAGTACCAAGAGGCGGCCATCACCGTAC  
 AGCGCAAGAGCTTCCCGACAGCAGCTTTATGTGGTGGTGGTGAAGACCGAAGACCAAGCTCGGGGGCT  
 CCCTGCCCTTCTACCCCTTCGACAGAGATGAACCGGTGATCAAGGGCACCGCCAGAAACCTGTGAGTGTGG  
 TGCTCAAGCAGTCAGTCTGAGGCATACGTGAGTGGATGCTCTTTGCTGGGTATATTTCTCTCCTTTTACC  
 TGCTGACCGCTCCTCTGGCCTGCTGGGAGAACTGGAGGACAGAGAAGAACCTGCTGGTGGCCATGACCGAG  
 CTGCCGAGAAAGCGGTACCCTCGAGTCTGGCTGATTCTTTCTGGCAGTTCCTTATGAGGGTTACAACT  
 ATGGCTCCTTTGAGATGTTTCTGATCTACCGATGGTCTGGTTGACAGCGCTGGCACTGGGGACCTCTCTTACG  
 GTTACAGGGCGGCTCTTTGAACCTGTAGTACTGCCGCCGAGTGGACTCATGAGCTCTGTGGAGGAGGATG  
 ACTACGACATTTAGCGACATCGATTCCGACAGAAATGTCAATGCAACCAAGCAATACCTCTATGTGGCTGACCT  
 TGGCAGAGGAGACAGAGCGGTGTTCTGCGGAAAAAGTACAGACTCTCTGGAACATTTGCCACATGCTGTCT  
 TCTATGCCCTTCTGTGGTGCAGCTGGTGATCACCTACCAAGCGGTGGTGAATGTACAGGGAATCAGGACATCT  
 GCTACTACAATTTCTCTGGCCGCCACCCACTGGGCAATCTCAGCGCTCTCACAACTCTCAGCAACCTGGGGT  
 ACTACCTGCTGGGGGCTGTTTTCTGCTCATCATCTGCAACGGAGATCAACACAGCTCCGCGGCTGCTGCGCA  
 ATGACCTCTGTGCCCTGGAATGTGGGATCCCCAAACACTTTGGGCTTTTCTACGCCATGGGCGACAGCCGTGATG  
 TGGAGGGGCTGCTCAGTGTGTGATCATGTGTGCCCACTATACCAATTTTCAGTTTGACACATCGTTCAATGT  
 ACATGATCGCGGACCTCTGCATGCTGAAGCTCTACCAAGCGGCAACCGGACATCAACGCGAGCGCTCAGAGT  
 CTACGCTGCTCGGCCATTTGCTATCTTCTCTCTGTGCTGGGCGTGGTCTTTGGCAAGGGAACAGCGGCTTCT  
 GGATCGTCTTCTCCATCATTCACATCATGCCACCTGCTCCTCAGCAGCAGCTCTATTACATGGCGCGGTGGA  
 AACTGGACTCGGGGATCTCCGCCCATCCTCCAGCTGCTACACAGACTGCATCCGGCAGTGCAGCGGGCCGCG  
 TCTACGTGGACCGCATGCTGCTGTGTCATGGGCAACGTATCACTGTCGCTGGCTGCCATGGGCTTATCA  
 TGGCCCCAATGATTTGCTTCTCACTTGTGGCCATTGGCATCTGCAACCTGCTCTTTACTTCGCCCTTACAC  
 TCATCATGAAGCTCCGAGTGGGAGAGGATCAAGCTCATCCCCCTGCTCTGCATGTTTTGACACTCCGTGGTCT  
 TGGGCTTCGCGCTCTTCTTCTTCCAGGGACTCAGCACTGGCAGAAACAGGCTGCAGAGTCGAGSGAGCAC  
 ACCGGGACTGCATCTCTCGACTCTTTGACGACCAGCATCTGGCACTTCTCTCTCCATCGCCATGTTTCG  
 GGTCTTCTCTGCTGTTGCTGACACTGGATGACGACCTGGATACTGTGAGCGGGACCAAGATCTATGTTCT~~TAGC~~  
 AGGAGCTGGGGCTTTCGCTTCACTCAAGGGGCCCTGAGCTCCTTTGTGTCATAGACCGGTCACTCTGTGCTGT  
 GTGGGATGAGTCCAGCAGCGCTGCCAGCACTGGATGGCAGGACAGAGGCTAGCTAGCTTAGGCTTGGCT  
 GGGACAGGCATGGGTGGCATGGAACCTTGCAGCTGCCCTCTGCCAGGACAGCGGCTGCTCCCTGGAAACCCCC  
 AGATGTTGGCAAAATTTGCTTCTTCTCAGTGTGGGGCTTCCATGGGCGCTGCTCTTTGGCTCTCCATT  
 GTCCTTTGCAAGGGAAGGATGGAAGGACACCTTCCCATTTTCATGCTTGCATTTTGGCCGCTCTCTCCCC  
 ACAATGCCCACTGGGACCTAAGGCTCTTTTCTCTCCATACTGCCACTCAGGGCTAGCTCGGGGCTGTA  
 ATCTCTGCTCTGTATCAGGGCCCCAGTTCTCTTTGGGCTGTCCCTGGCTGCCATCACTGCCCATTCAGTCAGCC  
 AGGATGGATGGGGTATGAGATTTTGGGGTTGGCGAGCTGGTGCCAGACTTTTGGTGTGTAAGGCTGCAAGGG  
 CTGGGGCGCTGCTATTTCTTCTCCTCTGACCTGTGTCTCAGGCTGGCTCTTTAGCAATGGGCTCAGGCCAAAT  
 TGAGAACCCGCTTGTGATTCAAGAGCTGAATTCAGAGGTCACTCTCATCCCATCACTGCCAGACTGACGC  
 AGCACAAGACTGGAGAGCAAGGCGCTCACCCCTCCTCTCTTTCTTTCAGGCGCTTAGTCTTGCCAAACCC  
 AGCTGTTGGCTTTTCACTGCCATTGACCTGCCAAGATGTCCAGGGGCAAGAGGGATGATACAGGTTTCAG  
 CCCGTTCTGCTCCAGCTGTGGGCAACCCAGTGCTTACCTTAGAAAGGGGCTCAGAGAGGATGTGCTGTTT  
 CCGCTCTAGTGGCCGCTCTAGCTCTGCTTAGCAACCCAGGCTGGCTCTAAGTTTTCGCTCCAGTCTGCTGAGCA  
 AGTTCTGTGTTAGTATGACGACACATACCTATGAACCTTGAAGTTTACAAAGAGTCCGCCCACTCTGGGCA  
 CTTGGCCACCTGGTCTTGGATCCCTTCTGCTCCAGCTGTGCCACCGAGTGTGAGGATGGGGAGCTCAGG  
 CGGGGCTCTGCTTTTGGGATGGGAATGTGTTTTCTCCAAACTGTGTTTTATAGCTCTGCTTGAAGGCTGGG  
 AGATGAGGTGGTCTGATCTTTTCTCAGAGCGCTCCTCATGCTATGGTGTGCTTCGTTTTCTATGAATGAAT  
 TGCATTCATAAACAACACAGACTCAAAAAA

**FIGURE 130**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESHGLVLPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNITYQLRVSRMDDFVLRRTGEQFSFNTAAQPOQYFKYEFEGVDSVI
VKVTSNKAFFPCSVISIQDVLCPVYDLNNAVIFIGMYQTMTKKAAITVQRKDFPSNSFYVVVV
VKTEDQACGGSLPFYPFAEDEPVDQGHRQKTLVSVLSQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLTLLVAIDRACPESGHPRVLADSFPGSSPYEGYNGSFENVSGSTDGL
VDSAGTGDLSYGYQGRSFEPVGTTRPRVDSMSSVEEDDYDTLTDIDSDKNVIRTKQYLYVADL
ARKDKRVLRRKKYQIYFWNIATIAVFYALPVVQLVITYQTVVNVNTGNQDICYNFLCAHPLGN
LSAFNNILNSLGYILLGLLFLLIILQREINHNRAILLRNDLCALECGIPKHFGFLFYAMGTALM
MEGLLSACYHVCPNYTNFQFDTSMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVFFS
VLGVVFGKGNATFVIVFSIIHIIATLLSTQLYYMGRWKLDSGIFRRILHVLYTDCIRQCSCG
PLYVDRMVLLVMGNVINWLSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI
KLIPLLCIVCTSVVWGFFALFFFFQGLSTWQKTPAESREHNRCILLDFDDHDIWHFLSSIA
MFGSFLVLLTLDDDDLTQVRDKIYVF
```

**Important features of the protein:****Signal peptide:**

amino acids 1-18

**Transmembrane domains:**

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

**Leucine zipper pattern.**

amino acids 497-518

**N-glycosylation sites.**

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

**FIGURE 131**

GCTCAAGTGCCTTGCCTTGCCCCACCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC  
 TCTCTTCTTGGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCCTGCTCGT  
 ACCATGGTCCCTGCTGCTGTGGCTGCTTGTGTCTCCGTCCCCAGGCTCTCCCCAAGGC  
 CCAGCCTGCAGAGCTGTCTGTGGAAGTTCCAGAAAATATGGTGGAAATTTCCCTTTTATACC  
 TGACCAAGTTGCCGCTGCCCGTGTAGGGGGGCTGAAGGCCAGATCGTGTCTCAGGGGACTCA  
 GGCAGAGCAACTAGGGCCCATTTGCTATGGATCCAGATTTCTGGCTTCCGTGCTGTGACCGA  
 GGCCCTGGACCGAGAGGAGCAGGCAGAGTACCAGCTACAGGTACCCCTGGAGATGCAGGATG  
 GACATGTCTTGTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTG  
 CCCCATTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGGTACCAGGCCTGGCATCCC  
 CTTCTCTTCTTCTTGGGCTTACAGCCGGGATGAGCCAGGCCACAGCCAACTCGGATCTTCGAT  
 TCCACATCTGTAGCCAGGCTCCAGCCAGCCTTCCCCAGACATGTTCCAGCTGGAGCCTCGG  
 CTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC  
 CTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACCAGGCCACTG  
 CCACCGTGGAAAGTCTCCATCAGAGAGCAGCTGGGTGTCCTAGAGCCTATCCACCTGGCA  
 GAGAATCTCAAAGTCTTATACCCGACCCACATGGCCAGGTACATGGAGTGGGGGTGATGT  
 GCATGTACCTGGAGAGCCTATCCCCCGGGACCCCTTTGAAGTGAATGCAGAGGGAAACCTCT  
 ACCTGACCAGAGAGCTGGACAGAGAAGCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG  
 AATTCCCATGGCAGGAGTATCGGCCCCCTCTGGAGCTGCACGTGCTGGTGTGATGGAATGAGAA  
 TGACAACGTGCTTATCTGCCCTCCCCGTGACCCACAGTCCAGCTACCTGAGCTCAGTCCAC  
 CAGGTACTGAAGTGACTAGACTGTGACGAGGAGTGCAGATGCCCCCGGCTCCCCAATTCC  
 CAGCTTGTGTATCAGCTCCTGAGCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTCCA  
 GGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCAGCAGGCCAGAACCA  
 TCCTGCTTCTGGTGTGCGCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCAGTGT  
 GAAGTCGAAGTCGAGTCACAGATATCAATGATCACGCCCCCTGAGTTCATCACTTCCAGAT  
 TGGGCCATATAAGCTCCTGAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCA  
 TTGATGCTGACCTCGAGCCCGCCTTCCGCCCTCATGGATTTTGCCATTTAGAGAGGGGAGACACA  
 GAAGGGGACTTTTGGCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTTGCAC  
 GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGA  
 AGCTGTTGGGGCCAGGCCAGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGA  
 GTGATGCCACCCCCAAGTTGGACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGCCCC  
 AGCCGGCTCTTTCTGCTGACCATCAGCCCTCCGACCCCATCAGCCGAACCTCAGGTCTCT  
 CCCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATCTCCGGGGAGGTGCACACC  
 GCGGACTCCCTGCAGGGCGCCAGCCTGGGGACACCTACACGGTGTCTTGGAGGGCCAGGA  
 TACAGCCTGACTCTTGCCCCCTGTGCCCTCCCAATACCTCTGCACACCCCGCCAGACCATG  
 GTTGATCTGTGATGAGCCAGCAAGGACCCGATCTGGCCAGTGGGACAGTCCCTACAGC  
 TTCACCTTGGTCCCAACCCACGGTGCAACGGGATTGGCGCTCCAGACTCTCAATGGTT  
 CCATGCTCACTCACTTGGCCCTGCATTGGGTGGAGCCAGTGAACACATAATCCCCGTGG  
 TGGTGCACCACAATGCCCCAGATGTGGCAGCTCTGGTTCAGTGATCTGTGTCTCGCTGCAAC  
 GTGGAGGGGACAGTCATCGCAGAGTGGGCGCATGAAGGGATGCCACGGAAGCTGTCTGGC  
 ACTGGGCATCCTTGTAGGCACCTGGTAGCAATAGGAATCTTCTCATCTCATTTTACACC  
 ACTGGACCATGTCAAAGGAAGAGGACCCGGATCAACCAGCAGACAGCGTGCCCTGAAGGCG  
 ACTGTCTCAATGCGCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAGTCCC  
 CTGGGAGAGAGCCAGCAGCCCAAGATCCAGCAGGGGACAGGACAGATAGAAGCCCTCCAT  
 CTGCCCTGGGGTGGAGGCACCATCACCATCACCAGGCATGTCTGCAGAGCCTGGACACCAAC  
 TTTATGGACTGCCCATGGGAGTGTCCAAATGTGAGGGTGTGTGCCCAATAATAAGCCCCCA  
 GAGAAGTGGGCTGGGCCCCATTTGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

**FIGURE 132**

MVPAWLWLLCVSVPAALPKAQAELSVSEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG  
 KATEGPFAMDPDSGFLLVTRALDREEQAQYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP  
 HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAPQSPDMFQLEPRL  
 GALALSPKGSTSLDHALERTYQLLVQVKMDGDAQSGHQATATVEVSIESTWVSLEPIHLAE  
 NLKVLPHHMAQVHWSSGGDVHYHLESHPPGPFVNAEGNLYVTRELDREAQAQYLLQVRAQN  
 SHGEDYAAPLELHVLVMDENDNVPICPPRDPTVSIPELSPPGTEVTRLAEDADAPGSPNSH  
 VVYQLLSPEPEDGVEGRAQVDPTSGSVTLGVLPRLAGQNILLVLAMDLAGAEGGFSSTCE  
 VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTADLEFAFRMLMDFAIERGDTE  
 GTFGLDWEPSDGHVRLRLCKNLSYEAAPSHEVVVVVQSAKLVGPGPGPGATATVTVLVERV  
 MPPPKLDQESYEASVPISAPAGSFLLLTIQPSDPISTRFLRSLVNDSEGWLCIEKFSGEVHTA  
 QSLQGAQPGDYYTVLVEAQDTALTAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF  
 TLGNPNTVQRDWRLQTLNGSHAYLTALHWHVEPREHIIPVVVSHNAQMWQLLVRVIVCRCNV  
 EGQCMRKVGRMKGMPTKLSAVGILVGTLVLAIGIFLILIFTHWTMSRKKDPDQPADSVPLKATV

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 762-784

**FIGURE 133**

CCGGGGACATGAGGTGGATACTGTTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA  
 GAAAAATTTTTTGGGGACCAAGTTTTGAGGATTAATGTCAGAAATGGAGACGAGATACGCAA  
 ATTGAGTCAACTAGTGAATTCAAACAACCTGAAGCTCAATTTCTGGAAATCTCCCTCCTCCT  
 TCAATCGGCCTGTGGATGTCCTGGTCCCATCTGTCAGTCTGCAGGCATTTAAATCCCTTCCTG  
 AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTTTAGACAAATGA  
 GATGATGAATGCAACAATGAAGGGCAAGAACGGAGCAGTAATTAACCTCAACTACGGGG  
 CTTACCATTCCCTGGAAGCTATTTACCACGAGATGGACAACATTGCCGCAGACTTTCCTGAC  
 CTGGCGAGGAGGGTGAAGATTGGACATTGCTTTGAAAACCGGCCGATGATGTAAGTGAAGTT  
 CAGCACTGGGAAAGCGGTGAGGCGGCCGCCGTTGGCTGAATGCAGGCATCCATTCCCGAG  
 AGTGGATCTCCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTAATCTGATTACGAGAG  
 GATCCAGCTATCACCTCCATCTTGGAGAAAAATGGATATTTTCTGTTGCCTGTGGCCAATCC  
 TGATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACCGCGTCCCGAAATC  
 CTGGAAGCTCCTGCATTGGTGCTGACCCAAATAGAACTGGAACGCTAGTTTTGCAGGAAAG  
 GGAGCCAGCGACAACCCCTGCTCCGAAGTGTAACATGGACCCACGCCAATTTCGGAAGTGGGA  
 GGTGAAATCAGTGGTAGATTTTCATCCAAAAACATGGGAATTTCAAGGGCTTCATCGACCTGC  
 ACAGCTACTCGCAGCTGCTGATGATCCATCTGGGTACTCAGTCAAAAAGGCCCCAGATGCC  
 GAGAACTCGACAAGGTGGCGAGGCTTGCGGCCAAAGCTCTGGCTTCTGTGTCTGGGCACTGA  
 GTACCAAGTGGGTCCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGG  
 CGTATGACAACGGCATCAAAATTTGCATTACATTTGAGTGTAGAGATACCGGACCTATGGC  
 TTTCTCCTGCCAGCTAACAGATCATCCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGAC  
 CATCATGGAGCATGTGCGGGACAACCTCTACTAGGCGATGGCTCTGCTCTGTCTACATTTAT  
 TTGTACCCACAGCTGCACGCACTGAGGCCATTGTTAAAGGAGCTCTTTCTACCTGTGTGAG  
 TCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCCTGCCCTCTCCAGCCAGCTCCCTGGAGT  
 CGTGTGCTCTGGCGGTGTCCTGCAAGAACTGGTTCTGCCAGCCCTGCTCAATTTTGGTCCTG  
 CTGTTTTTGTATGAGCCTTTTGTCTGTTTCTCCTCCACCCTGCTGGCTGGCGGCTGCACT  
 AGCATCACCCCTTCTGGGTGGCATGTCTCTCTACCTCATTTTTTAGAACCAAGAACATC  
 TGAGATGATTCTCTACCTCATCCACATCTAGCCAAGCCAGTGACCTTCTCTGGTGGCACT  
 GTGGGAGACACCACTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTTCTCTTAATTTT  
 TCGCAGTCTTCTGGAAAATATTTTCTTTGAGCAGCAAATCTGTAGGGATATCAGTGAAG  
 GTCTCTCCCTCCCTCTCTCTGTTTTTTTTTTTTTTTGGAGACAGAGTTTTGCTCTTGTGGC  
 CAGGCTGGAGTGTGATGGCTCGATCTTGGCTCACCAACCTCTGCTCTCTGGGTTCAGCA  
 ATTCTCCTGCCTCAGCCTCTTGTAGTAGCTTGGTTTTATAGGCGCATGCCACCATGCCTGGCTA  
 ATTTTTGTGTTTTTAGTAGAGACAGGGTTTTCTCCATGTTGGTCAGGCTGGTCTCAAACCTCCCA  
 ACCCTCAGGTGATCTGCCCTCCTTGGCCTCCACAGAGTGTGGGATATACAGGTGTGAGCCACTG  
 TGCCGGGCGGCTCCCTCCTTTTTTTAGGCCTGAATCAAAGTAGAAGTCACTTTCTTTAC  
 TGTGCTGAGAATTTCTAGATACTACAGTTCTTACTCCTCTCTTCCCTTTGTTATTCACTGTG  
 ACCAGGATGGCGGGAGGGGATCTGTGTCACTGTAGGTACTGTGCCAGGAAGGCTGGGTGAA  
 GTGACCATCTAAATTCAGGATGGTGAATTTATCCCATCTGCTCAATGGGCTTACCTCTCT  
 CTTTGCTTTTGAACCTCACTTCAAAGATCTAGGCCTCATCTTACAGGTCTTAATCACTCAT  
 CTGGCCTGGATAATCTCACTGCCCTGGCACATCCCCATTTGTGCTGTGGTGTATCTCTGTGTT  
 TCTTGTGCTGGTG  
 TCTGTCTATTTGTATCTCGACCACAAAGTTCTTAAGTAGAGCAAGAATTCATCAACGACTT  
 GCCTCTGTTTTTCATTTCACTCAGCAGTACCATCTGTCCTTTTGTGTTGTGTTGTGTTGTGTT  
 TTGTTTTTTTGTCTTTTACCAACATGTCTGTAATCTTAACCTCCTGCCTAGGATTTGTACA  
 GCATCTGGTGTGTGCTTATAAGCCAATAAATATTCAATGTGAAAAAAAAAAAAAAAAAAAA

MRWLIFIGALIGSSICQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKNLFWKSPSSFNR  
PVDVLVPSVSLQAFKSFRLSQGLEAYVTIEDLQALLDNEDDEMQHNEGQERSNNFNFGAYH  
SLEAIYHENDNIAADFPDLARRVKIGHSFENRMYVLKFSTGKGVRRPAVWLNAGIHSREWI  
SQATAIWTARKIVSDYQRDPAITSILEKMDIFLIPVANPDGYVYTQTQNRWLWRKTRSRNPGS  
SCIGADPNRNWNASFAGKAGDNPCSEVYHGHPANSEVEVKSVDVDFIQKHGNFKGFDILHSY  
SOLLMPYGYSVKKAPDAEELDKVARLAALASVSGTEYQVGTCTTVYPSAGSSIDWAYD  
NGIKFAFTFELRDGTGYGFLPANOIPTAEETWLGLKTI MEHVDRNLY

amino acids 1-16

[illegible]



**FIGURE 136**

MASYLYGVLFVAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE  
 TPSQNIFFSPVSVSTSLAMLSSLGAHSVTKTQILQGLGFNLTHTPESAIIHQGFQHLVHSLTVP  
 SKDLTLKMGSAFLVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQ GK  
 VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAF  
 GVDTELNCFVLQMDYKGDVAFFVLP SKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF  
 SISASYNLEITILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTT  
 KFIVRSKDGPSYFTVSNRTFLMMITNKATDGLFLGKVENPTKS

**Signal peptide:**

amino acids 1-20

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[illegible]

**FIGURE 138**

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATI  
 SGSSVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSE  
 SSTPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS  
 TTSSGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTT  
 SNGAGTATNSESSTTSSGASTATNSDSSSTVSSGASTATNSESSTTSSGASTATNSESSTTSS  
 GASTATNSDSSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGA  
 NTATNSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSSTTSSEAST  
 ATNSESSTVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAV  
 SEAKPGGSLVPWEIFLITLVSVVAAGVLFAGLFFCVRNLSLSLRNTFNTAVYHHPGLNHGLGP  
 GPGGNHGAHRPRWSPNWFWRFPVSSIAMEMSEGRNSGP

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 510-532

**FIGURE 139**

GGGAGAGAGGATAAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC  
 CCAGCAAT**ATG**CATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC  
 CTGTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGG  
 GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGAATCACGC  
 ATGCCGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGC  
 AAGGAGTTGGACAAGGCGCTCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT  
 CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG  
 CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCAC  
 CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG  
 AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC  
 TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACAGCTGCTGAATGGC  
 AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG  
 GGCCTCAGTCAACACGCCTTTCATCAACCTTCCCGCCTGTGGAGGAGCGTCGCCAACATCA  
 TGCC**TAA**ACTGGCATCCGGCCTTGTGGGAGAATAATGTCGCCGTTGTACATCAGCTGAC  
 ATGACCTGGAGGGGTTGGGGTGGGGGACAGTTTCTGAAATCCCTGAAGGGGTTGTACTG  
 GGATTTGTGAATAAACTTGATACACCA

**FIGURE 140**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG
REVEKVFNGLSNMGSHTKELDKGVQGLNHGMDKVAHEINHIGIQAGKEAEKLGHG VNNAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTFFINLPALWRSVANIMP
```

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**Homologous region to circumsporozoite (CS) repeats:**

amino acids 35-225

141/249

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[illegible]

**FIGURE 142**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962

><subunit 1 of 1, 837 aa, 1 stop

><MW: 92750, pI: 7.04, NX(S/T): 6

MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLQPPPTWALSPRISLPLGSEERPFLLRF  
EAEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEKKQQCSFKG  
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFS PMCTYINMENFTLARDEKGNVLEDDGKGRC P  
FDPNFKSTALVVDGELYTGTVSSSQNDPAISRSQSLREPTKTESSLNWLQDPAFVASAYIPE  
SLGSLQGDDDKIYFFFSETGQEFFEFNTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC  
SRPDDGFPPNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSACVFTMKDVQRVFSG  
LYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSQLPDRVLNFKDHFLLMDGQVR  
SRMLLLQPQARYQRVAVHRVPGLHHTYDVLFLGTGDGRLHKAVSVGPRVHIIIEELQIFSSGQ  
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSILYQP  
QLATRPWIQDIEGASAKDLCSSASSVVSPSFVPTGEKPCEQVQFPNTVNTLACPLLSNLATR  
LWLRNGAPVNASASCHVLPTGDLLLVTQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQ  
TDEGGSVPVPIISTSRVSAFAGGKASWGADRSYWKFEFLVMCTLFVLAVLLPVLFLLYRHRNSM  
KVFLKQGECA SVHPKTCPVVLPETREPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSEKR  
PLSIQDSFVEVSPVPCPRPRVRLGSEIRDSVV

**Transmembrane domains:**

amino acids 23-46 (type II), 718-738

**FIGURE 143A**

CTAAGCCGGAGGATGTGCAGCTGCGGCGCGGCGCGGCTACGAAGAGGACGGGGACAGGCGCCGTGCGAACCGA  
 GCGCCAGCAGCGCGGAGACGCGGCGAGGCGGGGACGGGAGCCCGGACTCGTCTGCCGCGCGCGTCTGCGCCGTG  
 TGCCGCGCCCGCTCCCCGCGCGGAGGAGCGCCGCACTTCGCGCCGCGCGCGCGCGCTTACGCGCGCGC  
 CGGGCATGTCTCCCTCTTAAAGCGCAGGCGCGCGCGCGCGGGCGGGTGTGCGGAACAAAGCGCGCGCGGGG  
 CCTCGGGCGCGCTCGGGGCGCCGATGGCGCGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG  
 CGGCGCTAGGCGCGGCTGGCTCCGTGGGCGGGGCGAGCGGGCTGAGGCGCGCGCGAGCTCGGCGCGGCGCGCG  
 GGGCGCGCGCGCGCGCGCGCGCGGGGAGCGCGCGGGGATGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG  
 TGCTCGGGCTCGCTCGCTGGGCTCTGTGCTGGCTCGCGGCTCTGCTCTGCGCCCGGGCTTCGAGCTGAAGCGAGCGC  
 GCCACGCGCGCGCGCGCGCGCGCGCGGGTGGCGGTGCGGGGAGCGCGCGCGCTCCGAGCGCGCGCGCGCGCG  
 GCGATGCGCGCGCGCGCGCGCTCTGGCGCGCGGGTCTGGAGCCAGATGGCGGCGCGCGCGAGGAACCTTCTCT  
 TCGTGGGAGCTGACGCGCCAGAAATACCTGCAGACTCGGGCCGTGGCGCGCTACAGAACATGGTCCAAGACAA  
 TTCTCGGGAAGTTGAGTCTTCTCAAGTGAGGTTCTGACACATCTGTACCAATTCCAGTAGTGCCACTACGGG  
 TGAACAGCAGCTGCGCCGCTGTTCTTGGGCGAGACGGCTGGGCAACGGAAGAAATGGGAAACGTGCCCTGG  
 AGCTTGTGAGAACTTCTGCATGGGGGGGCTGGCTGATCATGAGCGGGAGGTGCTTCGAGAACTTGTGGCGC  
 ACATTGGAGAGTGTCTCGGGAGATGTACACCAACCATGAGAGCTGGAGGTGGGAAGGTGTCTCGGAGGTTTG  
 CAGGGGTGAGTGTGTGTGTGTTATGAGATGCGCGAGCTTTTTTATGAGAATTACGAGCAGAACAAAGAGGGT  
 ACAGTTAGAGATCTCCATAAGCAGTAAATTCACCAAGCTATACATTACACCCCAAAAACCCACCTACCGCT  
 ACAGGCTTCCACAGCTACATGCTGAGCCGAGATATCCGAGCTCCGCACTCGCACTACAGCTGCACGCGGAA  
 TTGTCTGATGAGCAATAACAGCAACAGAAATTCATAAAGAGGACCTCGAGCTGGGAATCCCTCCCTCCCTCA  
 TGAGGTTTCAGCCCGCGGACGAGGAGATTCGGAATGGGATTTCTGACTGGAAATATCTGTATTGGCAG  
 TTGACGGCGAGCCCTTCGAGAGGAATGAGTCTCGGCCAGAGGAGGCGCTGGAGCAGCATTTGTCATGAGCTCA  
 TGGAGATGATCAATGCGAGCGGACGAGGCGCGCATGTTGACTCAAGAGATGACAGCACTACGCTACCGC  
 GGTTGAACCCCATGTATGGGCTGAGTACATCTGGAGCTGCTGCTTCTGTACAAAGGACCAAGGGAAGAA  
 TGACGCTCCCTGTGAGGAGGACGCGTATTTCAGCAGAGCTTTCAGCAAAATCAGTTTGTGGAGCTGAGGAGC  
 TGGATGCACAGAGTTGGCCAGAGAAATCAATCAGGAATCTGGATCCTGTGCTTCTCTCAAACTCCCTGAAGA  
 AGCTCGCCCTTTCAGCTCCCTGGGTCGAGAGTGAGCACAAGAACCCAAAGATAAAAGATAAACATATGA  
 TTCTTTGTCTGGGCGTTTCGACATGTTTGTGAGATTTATGGGAACTTGTAGAAGACGTGTTATCCCCAATC  
 AGAAGCTCAAGCTCGTGTTCTGCTTTTCAATTCTGACTCCAACCTGACAAAGGCAACAAAGTTGAATGATGA  
 GAGATTACCGCATTAAGTACCTTAAAGCCGACATCGAGATTTGCTGTGTCTGGAGAGTTTCAAGAGCCCTGG  
 CCCTGGAAAGTAGGATCTCCAGTTTAAACATGAATCTTTGCTCTTCTTGCAGCTCGACCTCGTGTTTTACTA  
 CAGAAATCTCTCAGCGATTCGAGCAAAATACAGTTCTGGGCGCAACAAATATATTTTCCAATCATCTTCAGCCAGT  
 ATGACCCAAAGATTGTTTATAGTGGGAAAGTTCCAGTGACAACCAATTTTGGCCTTACTCAAGAAATCTGCTCT  
 GGAGAACTATGGGTTTGGCATCAGTGATTTATAAGGGAGATCTTGTCCAGTGGGTGGCTTGTATGTTTCCA  
 TCCAGGCTGGGCGCTGAGGATGTGGACCTTTCAACAAGGTTGTCCAGGAGGTTTGAAGAGCTTTAGGAGCC  
 AGGAAGTAGGAGTAGTCCAGCTCCACCATCTGTCTTTGTGATCCCAATCTTGACCCCAACAGTACAAATGT  
 GCTTGGGCTCCAAAGCATCGACATCTGGGTCCACCCAGCAGCTGGCTGAGATGTGGCTGGGAAAAAATGATCCAA  
 GTTACAGCTAAAAGCAGCAATAATAATGGCTCAGTGAGGACAGCGCTAATGTCAGGCTTGTCTGGAAAGAGCGTTT  
 TAAATATCTAATTTTTTTTCAAAATTTTTTGTATGATCAGTTTTTGAAGTCGATATACAGGATATATTTTTAC  
 AAGTGGTTTTCTTATACAGGACTCTTTTAAAGTGTGAGTCTTCTGAACAAGAGGATGATCAGTGTGTGCTTTGAA  
 CACATCTTCTTGTGCAACATTTGTAGCAGACCTGCTTAACTTTGACTTGAATGTACCTGATGAACAAACTTT  
 TTTAAAAAATGTTTTCTTTGAGACCTTTGTCTCAGTCTATGCGCAGAAAGCTGAACATCTCTCGCAAGAT  
 TATTGTAAACAAACAGCTGTAACCTGCTGAATGTTCTGTTGATTGTTAACTTCCAGATTTCTACTTTTGT  
 GTTTGTTTTTTTTTTTACAATTTGTTTAAAGCCATTTCAATGTTCCAGTTGTGAAGATAAGGAATCTGATAATA  
 GCTGTTTCAATCTGCTCTCAGAGAGCTTTCAGAGTTGATCATTTCTCTCATGTACTCTGCTCAGCATGGC  
 CAGTAGGTTTTTGTGTTTTGTTTTGTTGTTCTTTTGTAGACGGAGTCTCATCTGTTACCCAGGCTGGAATG  
 CAGTGGCGCAATCTGGCTCACTTTAAACCTCACTCCCTGCTTCAAGCAATCCCTGCCCTTGCCTCCGAGT  
 AGCTGGGATACAGGCACACACCACGCGCCAGTATGTTTTTTGTATTTTGTAGAGACGGGGTTCACCAT  
 GCAAGCCAGCTGGCGCGCTAGGTTTTTAAAGCAAGGGCGGTGGAAGAGGCACATGAGTGTGTGCTGTCTG  
 TGGTAGTTTCAATGGCCCTAATAGACCTGGCATTAATTTTCAAGAGGATTTGACATTTTCTCTCTGACCTT  
 CTCTTTAAAGGGTAAAAATTAATGTTTGAATGACAAAGATGAATTTATGCAATAAACTGATGTACACAGAT  
 GAAACATACACATACACCTAAACAAAACGTTGGGGAAGAAATGTAATTTGTTTTGTTCTTCTTCACTCTGCTG  
 TGTATGTGGGTGGAGATGTTTTTCACTTCTTCACTACTGTGTTTATCTTTGTTATCTTTGATCTGAAATACCTTAA  
 TTTATTTAATATCTGTTGTTTCAGAGCTCTGCCAATTTTCTTGTAGTACTGTTTAGTTTAGTTATTTATTTGATGATCGG  
 GAGTGTGTTTAGTCTGTTTTATTTCGATTAACCGATCTCCAAAGATTTCCTTTTGAAGACGCTTTTTCCCTCC



**FIGURE 143B**

**FIGURE 144**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836

><subunit 1 of 1, 802 aa, 1 stop

><MW: 91812, pI: 9.52, NX(S/T): 3

MAAGRRRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR  
GDARGAQLWPPGSDPDGGPRDRNFLFVGVMTAQKYLQTRAVAAAYRTWSKTI PGKVQFFSSEG  
SDTSVPPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEFWMRADDVYIKGDRLENFLR  
SLNSSEPLFLGQTGLGTTEEMGKLALEPGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYT  
THEDVEVGRCVRRFAGVQCVCWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP  
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQPRQEE  
ILEWEFLTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY  
GYRRVNPMYGAEYILDLLLLYKKHKGKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR  
INQESGSLSFLSNSLKKLVFPQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFEKTC  
LIPNQNVKLVLLFNDSNPDKAKQVELMRDYRIYKPKADMQILPVSGEFSRALALEVGSSQ  
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFT  
QKTGFWRNYGFGITCIYKGDIVRVGGFDVSIQGWGLEVDVLFNKVVQAGLKTFRSQEFGVVH  
VHHPVFCDPNLDPKQYKMCGLGSKASTYGSTQQLAEMWLEKNDPYSKSSNNNGSVRTA

**Signal peptide:**

amino acids 1-23

**FIGURE 145**

GGACAACCGTTGCTGGGTGTCCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC  
 TTTCGGCCTTGAGGTTCCCAGCCTGGTGGCCCCAGGACGTTCCGTCGCATGGCAGAGTGCT  
 ACGGACGACGCCT**ATGA**AGCCCTTAGTCTTCTAGTTGCGCTTTTGCTATGGCCTTCGCTG  
 TGCCGGCTTATCCGAGCATACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATA  
 CAAGTTTTAGAGAACCTAGTACGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAATC  
 TAACTCTCCAAAACATGTTTATTCTATAGCATCAAAGGGATCAAATTTAAGGAGCTAGTTA  
 CACATGGAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAAATACA  
 ACTTTCCCTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAACACACGGAAAGTACCCC  
 ATCTGGTCGATCAAACCAAACATGTTTCCATGTGTTTGGCATGCAGAGGAACCTTATATTG  
 AAAATGAAGAGCCAGAGCCAGAGCCGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATG  
 TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTAC  
 CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT  
 CAGGTGAAACTGCGATAGAAAAACCCGAAGAGTTTGGAAAGCACCCAGAGAGTTGGAATAAT  
 GATGACATTTGAAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACTTCTTAGTGA  
 CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACGTAAACGAAGCC  
 TTGCTCTAGCAGCAGCAGCAGAACATAAATTAAAAACAATGTATAAGTCCAGTTATTGCCA  
 GTAGGACGAACAAGTAATAAAATTGATGACATCGAACTGTTATTAAACATGCTGTGTAATTC  
 TAGATCTAAACTCTATGAATATTTAGATATTAATGTGTTCCACCAGAGATGAGAGAAAAAG  
 CTGCTACAGTATTCAATACATTAATAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA  
 AAAGTTTAT**TAA**ACAATAATATAAAAAATTTAAACCTACTTGATATTCCATAACAAAGCTGA  
 TTTAAGCAAACTGCATTTTTTCACAGGAGAAATAATCATATTGTAATTTCAAAGTTGTAT  
 AAAAAATATTTCTATTGTAGTTCAAATGTGCCAACATCTTTATGTGTATGTTATGAACA  
 ATTTTCATATGCACATAAAACCTAATTTAAATAAAAATTTTGTTTCAGGAAAAA

**FIGURE 146**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864

><subunit 1 of 1, 350 aa, 1 stop

><MW: 39003, pI: 5.59, NX(S/T): 1

MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRVSPSGEPGREKKSNSPK  
HVYSIASKGSKFKELVTHGDASTENDVLTNPISSEETTTFTGGFTPEIGKKKHTESTPFWSI  
KPNNSIVLHAEPPYIENEPEPEPEPAAKQTEAPRMLPVVTESSTSPYVTSYKSPVTTLDK  
STGIEISTESEDPVQLSGETAIEKPEEFGKHPESWNDDILKKILDINSQVQQALLSDTSNP  
AYREDIEASKDHLKRSLALAAAAEHKLKTMYSQLLPVGRTSNKIDDIETVINMLCNSRSKL  
YEYLDIKCVPEMREKAATVFNTLKNMCRSRRVTALLKVY

**Signal peptide:**

amino acids 1-19

**FIGURE 147**

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTG  
 ACCTCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTCATAGTGTGAGATCAACCACAA  
 GGAATATCCATGGCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACA  
 GTGGCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCT  
 CCTGCTCCCTCTTTTCCTGAGACCAGTGCAGAGGCTATGGAAGTGC GGTTCTTCAGGAATCAG  
 TTCCATGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACA  
 GTATCGAGGGGAGAACTGAGTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTCTAAGGC  
 TAAAAAACATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTTCAGTTCCAGATTTAC  
 GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCCAT  
 CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCTCTCAGGCTGGTCCCCCAGC  
 CCACAGCCAAGTGGAAAGGTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAAATGCA  
 GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAAATGCTGGGAGCAT  
 ATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAG  
 AGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGT  
 GCCCTGTGTGGTGTGTGTCATGGGGATGATAATTGTTTTCTTCAAATCCAAAGGGAAAAATCCA  
 GGCGGAACTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCCGAAACACG  
 CAGTGGAGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAA  
 ACTGTAACCCATAGAAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAGAGATTTACAAGGAA  
 GAGTGTGGTGGCTTCTCAGGTTTCCAAGCAGGAGACATTACTGGGAGGTGGAGCTGGGAC  
 AAAATGTAGGGTGGTATGTGGGAGTGTGTCGGGATGACGTAGACAGGGGGAAGAACATGTG  
 ACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTCAC  
 ATTCAAATCCCCATTTTATCAGCCTCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCC  
 TGGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACC  
 CTGCTGACATGTCAGTTTGAAGGCTTGTGTGAGACCCTATATCCAGCATGCGATGTATGACGA  
 GGAAAAGGGGACTCCCATATTTATATGTCCAGTGTCCCTGGGGATGAGACAGAGAAGACCCTG  
 CTTAAAGGGCCCCACACCACAGACCAGACACAGCCAAGGGAGAGTGTCCCCGACAGGTGGC  
 CCCAGCTTCTCTCCGGAGCCTGCGCACAGAGAGTCACGCCCCCCTCTCTCTTTAGGGAGC  
 TGAGGTTCTTCTGCCCTGAGCCCTGCAGCAGCGGAGTCACAGCTTCCAGATGAGGGGGGAT  
 TGGCCTGACCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCA  
 CATTAGGTTTGTGTTTGTGAAAACCTCCATCCAGCTAAGCGATCTTGAACAAAGTCACAACCTCC  
 CAGGCTCCTCATTTGCTAGTACGGACAGTGATTCTCTGCCTCACAGGTGAAGATTAAGAGA  
 CAACGAATGTGAATCATGCTTGCAGGTTTGGAGGCACAGTGTTTGTCTAATGATGTGTTTTTA  
 TATTATACATTTTCCACCATAAACTCTGTTTGCTTATTTCCACATTAATTTACTTTTCTCTA  
 TACCAAAATCACCATGGAATAGTTATTGAACACCTGCTTTGTGAGGCTCAAAGAAATAAAGAG  
 GAGGTAGGATTTTCTACTGATTTCTATAAGCCAGCATTTACCTGATACCAAAACACGGCAAAG  
 AAAACAGAGAAGAGGAAGGAAAACACAGGTCCATATCCCTCATTAAACAGACACAAAAA  
 TTCTAAATAAAATTTAAACAAATAAACTAAACAATATTTAAAGATGATATATAACTACT  
 CAGTGTGGTTGTCCCACAAATGCAGAGTTGGTTTAATATTAAATATCAACCAAGTGTAAAT  
 CAGCACATTAATAAAGTAAAAAGAAAACATAAAAAA

**FIGURE 148**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866  
><subunit 1 of 1, 466 aa, 1 stop  
><MW: 52279, pI: 6.16, NX(S/T): 2  
MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA  
VVHLYRDGEDWESKQMPQYRGRTFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE  
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGY  
SLYDVEISIIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPPSPWRLASILLGLLGCALC  
GVVMGMIIVFFKSKGKIQAELDWRKKGQAELRDARKHAEVETLDPETAHPKLCVSDLKTVT  
HRKAPQEVPHSEKRFTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDVRGKNNVTLS  
PNNGYWVLRLTTEHLYFTFNPHFISLPPSTPPTRVGFLDYEGGTISFFNTNDQSLIYTLTLT  
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 131-150, 235-259

**FIGURE 149**

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTA  
 GGAAAAGAGTTTGTGGGAACCCCTGGGTTATCGGCCCTCGTCATCTTCATATCCCTGATTGTC  
 CTGGCAGTGTGCATTGGACTCACTGTTTATTATGTGAGATATAATCAAAGAAGACCTACAA  
 TTACTATAGCACATTGTCATTTACAACAGACAACTATATGCTGAGTTTGGCAGAGAGGCTT  
 CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAATAATGCATTTTATAAA  
 TCTCCATTAAAGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG  
 AGTGTGGCTCATATGCTGTTGATTGTAGATTTCACCTCTACTGAGGATCCTGAAACTGTAG  
 ATAAATTTGTTCAACTGTTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTA  
 GATCCTCACTCAGTTAAATTTAAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA  
 TTGCTGCGGAACACGAAGAAGTAAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAG  
 AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGT  
 GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTTTACAACATATAA  
 GAACCTGCCAGATGGACTGCTTCCCTTGGAGTAACAATAAAACCTTCGAAAATGAACGGG  
 GTCTCCGGAGAATAATTGTCATGAAAAATACAAACACCCATCAGATGACTATGATATTTCT  
 CTGCGAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGA  
 TGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAA  
 ATGATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAAC  
 TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT  
 AGAAGGAAAAACAGATGCATGCCAGGGTGAAGTCTGGAGGACCACTGGTTAGTTAGATGCTA  
 GAGATATCTGGTACCTTGTGGAATAGTGAGCTGGGAGATGAATGTGCGAAACCAACAAG  
 CCTGGTGTATATACTAGAGTTACGGCCTTGCGGGACTGGATTACTTCAAAACTGGTATCTA  
 AGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTTGTTTTTTTGGGTGTGGAGGCCATT  
 TTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAAC  
 TGTTTGTGTTGATGCATGTATTTCTTCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG  
 CCAGATCAACTCTGTCATCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATA  
 ATACAATATTACATTACAGCCTGTATTTCATTGTTCTCTAGAAGTTTGTGAGAAATTTGAC  
 TTGTTGACATAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTTCTTCAGTTCCCTC  
 AGCTCCTCTCATTTTCAAGCAATATCCATTTTCAAGGTGCAGAAACAGGAGTGAAAGAAAATA  
 TAAGAAGAAAAAATCCCTACATTTTATTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGT  
 GGAATATTAGAAATGATCATATTCATTATGAAAGGTCAAGCAAGACAGCAGAATACCAATC  
 ACTTCATCATTTAGGAAGTATGGGAACCTAAGTTAAGGAAGTCCAGAAAGAAGCCAAGATATA  
 TCCTTATTTTTCATTTCACAACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTG  
 ACCTATAATAATTATACAACTTCATGCAATGTACTTGTCTAAGCAAATTAAGCAAATAT  
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

**FIGURE 150**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYSTLSFTTD
KLYAEFGREASNFTSEMSQRLESMVKNAFYKSPLEEFVKSQVIKFSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEWFWQASLQWDGSHRCGATLINATWLVSAAHCFITYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVVPTNAVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSQNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI
```

**Transmembrane domain:**

amino acids 21-40 (type II)



**FIGURE 151**

GTCGAAGGTTATAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA  
 CAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCACAGACGTGAGCTGGTGGATTCCCG  
 CTGCATCAAGGCCTACCCACTGTCTCC**ATG**CTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC  
 CGTGACCTTCTTGGTTCCAGAGCTCAGCCCTTGCCCCCTCAAGACTTTGAAGAAGAGGAGG  
 CAGATGAGACTGAGACGGCGTGGCCGCTTTGCCGGCTGTCCCTGCGACTACGACCACTGC  
 CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCCGGCGGCTGCCTGTGCCC  
 AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCGCATGGGAGAAGTGCGCATTGCGG  
 CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCGGTCTCCACTACTGG  
 CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCCCGCTGAACGCTACGGTCCG  
 CAGAGCCGAAGTGAAGGGGCTGAAGCCAGGGGGCATTATGTCGTTTGCGTAGTGCCCGCTA  
 ACGAGGCCGGGGCAAGCCGCGTGTCCCGAGGCTGGAGGAGAGGGCTCGAGGGGGCCGACATC  
 CCTGCTTTCGGGCTTGACAGCCGCTTGCGGTGCCGCCCAACCCCGCACTCTGGTCCACGC  
 GGCGCTCGGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT  
 GCCTGCGGATCGCTGGGGCTGCCCCGCCGAGCCGCCGCCGAGCCGCAGGGGCGCT**CTGA**  
 AAGGGGCTGGGGGCATCTCGGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCCG  
 GGAAAGAGGAAAACCCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGGAGCCAGCCCCAG  
 GCTCCAGGGCCACGGCGGAGTCATGGTTCTCAGGACTGAGCGCTTGTTTAGGTCCGGTACTT  
 GCGCCTTTGTTTCTGGCTGAGGTCTGGGAAGGAATAGAAAGGGGCCCCCAATTTTTTTAA  
 AGCGGCCAGATAATAAATAATGTAACCTTTGCGGTTAAAAAAAAAAAAAAAAAAAA

**FIGURE 152**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874  
><subunit 1 of 1, 238 aa, 1 stop  
><MW: 25262, pI: 6.44, NX(S/T): 1  
MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEEADETETAWPPLPAVPCDYDHCRLQVPCKE  
LQRVGPAACLCPLGLSSPAQPPDPPRMGEVRIAAEEGRAVVHWCAPFSPVLHYWLLWLDGSEA  
AQKGPPPLNATVRRaelKGLKPGGIYVVCVVAANEAGASRPQAGGEGLEGADIPAFGPCSRL  
AVPPNPRTLVAHAVGVGTALALLSCAALVWHFCLDRWGCPRRAAARAAGAL

**Important features of the protein:****Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 194-220

**N-glycosylation site.**

amino acids 132-135

**FIGURE 153**

AGAGAAAGAACGCTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC  
 CTGCCCCGATGAGCCCCCGCGTGCCTGCCGACTATCCCAGCGGGCGTGGGGCACCGGG  
 CCCAGCGCCGACGATCGCTGCCGCTTTTGCCCTTTGGGAGTAGGATGTGGTGAAGGATGGGGC  
 TTCTCCCTTACGGGGCTCACAAATGGCCAGAGAAGATTCCTGTAAGTGTCTGCGCTGCCTGCT  
 CTACGCCCTCAATCTGCTCTTTTGTTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGGA  
 TGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTC  
 ATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGCTGTTTCCCTTATCAT  
 TGTGGGGATGTTAGGATATTGTGGAACGGTGAAGAAATCTGTTGCTTCTTGCAATGGTACT  
 TTGGAAGTTTGTCTGTCATTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAG  
 GAACTTATGGTTCAGATCAATGGTCAGATATGGTCACTTTGAAAGCCAGGATGACAAATTA  
 TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGAATTTTTTCAGAGAGAGTTTAAGT  
 GCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCAGAT  
 TCCTGCTGTGTTAGAGAATTCACAGGATGTTCCAAACAGGGCCACCAGGAAGATCTCAGTGA  
 CCTTTATCAAGAGGGTTGTGGGAAGAAATGTATTCCTTTTGGAGGGAACCAACCACTGC  
 AGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAATCCTGGCCATGATTCTCACC  
 ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAATGATGTC  
 CTTGAAGAATGACAACTCTCAGCACCTGTCACTGTCCTCAGTAGAACTGTTGAACCAAGCC  
 TGTCAAGAATCTTTGAACACACATCCATGGCAACAGCTTTAATACACACTTTGAGATGGGAG  
 GAGTTATAAAGAAATGTACAGAGAAGAAACCAAACTTGTTTTATTGGACTTGTGAATT  
 TTTGAGTACATACTATGTGTTTCAGAAATATGTAGAATAAAAAATGTTGCCATAAAATAACA  
 CCTAAGCATATACTATTCTATGCTTTAAATGAGGATGGAAAAGTTTCATGTCTAATGTCAC  
 CACCTGGACAATAATTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC  
 CTGTGTATGACTTTTACTGAACACAGTTATGTTTGGAGCAGCATGGTTGATTAGCATTTT  
 CGCATCCATGCAACAGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTACTT  
 CTACCACTAGTATATAAAGTACTAATTAATGCTAACATAGGAAGTTAGAAAATACTAATA  
 ACTTTTATTACTCAGCGATCTATTCTCTGATGCTAAATAAATATATATACAGAAAATTTT  
 AATATTGGTGACTACCTAAATGTGATTTTGTGTTTACTAAATATTTCTTACCCTTAAAA  
 GAGCAAGCTAACACATTTGCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAA  
 TCTGTATAATTCACTCGATTTTCACTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAA  
 ATTTGTCCTGTATAGCATCATTATTTTACGCTTTCTGTTAATAAAGCTTTACTATTCTGT  
 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAAACCAATTTTGAATAATA  
 CCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTAATA  
 GAAAATTTGCACATAACTTAGTTGATTGAGAAAGGACTGTGATGCTGTTTTCTCCCAATG  
 AAGACTCTTTTGGACACTAAACACTTTTAAAAAGCTTATCTTTGCTTCTCCAAACAGAA  
 GCAATAGTCTCCAAGTCAATATAAATCTCAGAAAAATAGTGTCTTTTCTCCAGAAAAAT  
 GCTTGTGAGAATCATTAACATGTGACAAATTTAGAGATTCTTTGTTTATTTCAGTGATTA  
 ATATACTGTGGCAATATACAGATTATTAATTTTTTACAGAGTATAGTATATTTATT  
 GAAATGGGAAAAGTGCAATTTTACTGTATTTTGTATTTTGTATTTTCTCAGAATATGGAA  
 AGAAATTAATGTGCAATAAATATTTCTAGAGAGTAA

**FIGURE 154**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880
><subunit 1 of 1, 305 aa, 1 stop
><MW: 35383, pI: 5.99, NX(S/T): 0
MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQ
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREF
PGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL
YYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL
```

**Signal peptide:**

amino acids 1-33

**Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248

**FIGURE 155**

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCGTGCCC  
 TGCACCTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGA  
 CCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAG  
 ACCGGGAGGATCACAGAGCCAGC**ATG**TTACAGGATCCTGACAGTGATCAACCTCTGAACAGC  
 CTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGAT  
 CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGCTCCTCATCAAGG  
 TGATTCTGGATAAACTACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCAGGAAGCAG  
 CTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT  
 CCCCAGAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG  
 ACTCGGCCACAGGGAAGTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAG  
 ACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGA  
 TGTGTGTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACCTCAAGTGGGGCCTGTC  
 TCTCAGGCTCCTGGTCTCCCTGCACGTCTTGCTGTGGGAAGAGCCTGAAGACCCCCGT  
 GTGGTGGTGGGGAGGAGCCTCTGTGGATTCTTGCCCTTGCCAGGTGAGCATCCAGTACGA  
 CAACAGCACGCTGTGTGGAGGGAGCATCCTGGACCCCACTGGGTCTTCACGGCAGGCCACT  
 GCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGGC  
 AGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATTTGAATTCAACCCCATGTACCCCCAA  
 AGACAATGACATCGCCCTCATGAAGCTGCAGTTCCTCACTCACTTTCTCAGGCACAGTCAGGC  
 CCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGA  
 TGGGGCTTTACGAAGCAGAAATGGAGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCA  
 GGTCAATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAGGGGGAAGTCAACCAGAGAAG  
 TGATGTGTGCAGGCATCCCAGGAGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCC  
 CTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGG  
 GGGCCCAGGACCCCAAGGATATACACCAAGGCTCAGCCCTATCTCAACTGGATCTACAATG  
 TCTGGAAGGCTGAGCTG**TAA**TGCTGCTGCCCTTTGTCAGTGTGGGAGCGCTTCTTCTCTG  
 CCTGCCCACCTGGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCTTGGGTACACCC  
 CTCTGCCACAGCCTCAGCATTTCTTGAGCAGCAAAGGGCCTCAATTCTGTAAAGAGACCC  
 TCGAGCCCCAGAGCGGCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCC  
 AGCATCCCAGGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA  
 GGAACCTTCCCCACACTACTGAATGGAAGCAGGCTGTCTTGTAAGGCCAGATCACTGTGGG  
 CTGGAGAGGAGAAGGAAAGGCTGCGCCAGCCCTGTCCGTCTTACCCATCCCCAAGCCTA  
 CTAGAGCAAGAAACAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTT  
 ACCTACTGTTGTCATTGTTATTACAGCTATGGCCACTATTATTAAGAGCTGTGTAACATCT  
 CTGGCAAAAAAAAAA

**FIGURE 156**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSQPLNSLDVKPLRKPRIPMETFRKVGIPITIIALLSLASIIIVVLIKVILDKYYF
LCGQPLHFI PRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWF
SACFDNFTEALAEACRQMGYSRAVEIGPDQDL DVVEITENSQELMRNSSGPCLSGSLVSL
HCLACGKSLKT PRVVGEEASVDSWPQVSIQYDKQHVC GGSILDPHWLTAACFRKHTDV
FNWKVRAGSKLGSFPLAVAKIIIEFNPMYPKDN DIALMKLQFPLTFSGTVRPICLPFFD
EELTPATPLWII GWGFTKQNGGKMSDILLQASVQVIDSTRCNAD DAYQGEVTEKMM CAGIPE
GGVDTCCQGD SGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAE L

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**Transmembrane domain:**

amino acids 32-53 (typeII)

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**FIGURE 157**

GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAACGACGCGGCATCCCCAGGCTCCAG  
 AGCTCCCTGGTGACAGTCTGTGGCTGAGC**ATG**GCCCTCCAGCCCTGGGCCCTGGACCCTGGAGCCTCCTGGGCC  
 TTTTCTCTTCCAACTGCTTCAGTGCTGCTGCCACGACGACCGCGGGGGGAGCGCGGCAGGGGCCATGCCCCA  
 GGGTCAGATACTATGCAGGGGATGAACGTAGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA  
 CTCTGCTCCTGAGTGGGTGATGGAAATACTCTCTACGTGGGGCTCGAGAAGCCATTCTGGCCCTGGATATCCAGG  
 ATCCAGGGGTCGCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTA  
 AGAAGAAGAGCAATGAGACACAGTGTTCACCTTCATCCGTGTCTGGTTTCTTACAAATGTCACCCATCTCTACA  
 CTTGCGGCACCTTCGCTTCAGCCCTGCTTGACCTTCATTGAACITCAAGATTCTTACCTGTTGCCCATCTCGG  
 AGGACAAGGTCAATGAGGGAAAAAGCCAAAGCCCTTTGACCCGCTCACAAGCATACGGCTGTCTTGGTGAGTG  
 GGATGCTCTATTCTGGTACTATGAACAACTTCTGGGCACTGAGCCCATCTGATGCGCACACTGGGATCCGAGC  
 CTGTCTCAAGACCGACAACCTTCTCCGCTGGCTGCATCATGACGCTCCTTTTGGCAGCCATCCCTTCGACCC  
 AGGTGCTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG  
 CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAGCTGCTGCAGAAAGTGGACCACTTCTTGAAGGCCAGC  
 TGCTCTGCACCCAGCGGGGCACTGCCCTTCAAGCTCATCCGCCACGCGGTCTGCTCCCGCCGATTTCTCCA  
 CAGCTCCCCACATCTACGAGTCTTCACCTCCAGTGGCAGGTTGGCGGGACAGGAGCTCTGCGGTTTGTGCCT  
 TCTCTCTCTTGGACATTGAACGTGTCTTAAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTA  
 CTTATAGGGGCCCTGAGACCAACCCCGGCCAGGCACTGCTCAGTGGGCCCTCCTCTGTATAAGGCCCTGACCT  
 TCATGAAGGACCACTTTCGTAGTATGAGCAAGTGGTGGGACGCCCTGCTGGTGAAATCTGGCGTGGAGTATA  
 CAGGCTTGCAAGTGGAGACGCCAGGGCCTTGATGGGCACAGCCATCTTGTCATGTACCTGGGAACACCACAG  
 GGTGCTCCACAAGGCTGTGGTAAAGTGGGACAGCACTGCTCATCTGGTGGGAAGAGATTGAGCTGTTCCTGACC  
 CTGAACCTGTTTGCACACTGCAGCTGGCCCCACCCAGGGTGCAGTGTGTTGTAGGCTTCTCAGGAGTGTCTGA  
 GGGTGCCCCGAGCCAACCTGTATGTCTATGAGAGCTGTGTGAGCTGTGTCCTGCCCGGACCCCACTGTGCCT  
 GGGACGCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACTGAACTCTTGAAGCAGCACTGAGATCCGAGCGG  
 GGAACCCAGAGTGGCATGTGCCAGTGGCCCATGAGCAGGAGCCTTCGGCTCAGAGCGCCCGCAAAATCATTA  
 AAGAAGTCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCTGCCCCAACCTGTGACGCTTGGCTCTTATTATT  
 GGAGTCAAGGCCAGCAGCACTCCGAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTCTTGCTGTATGATGAGCAGG  
 ATGGAGTTGGGGCTCTCTACCACTGCTGGGCAACTGAGAATGGCTTTTACATCCCTGTGATCTCTGATGGGTGG  
 ACAGCCAGGACCAAGCCCTGGCCCTGGATCCTGAACCTGGCAGGCACTCCCCGGGAGCATGTGAAGGTCCGTTGA  
 CCAGGGTCAGTGTGGGGCGGCCCTGGCTGCCAGCAGTCTTACTGGCCCCACTTTGTCACTGTCACTGTCTCTT  
 TTGCCTTAGTGCTTTTCAAGAGCCCTCATCATCTCGTGGCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGG  
 TTAGGCTGTGAGAACCTTGCGCCCTGGGGAGAAGGCCCTTGAAGCAGAGCAACCACTCCAGTCTCCCAAGG  
 AATGCAGGACCTCTGCCAGTGTATGTGGACGCTGACAACTGCCTAGGCACTGAGGTAGCT**TAA**ACTCTAGGCA  
 CAGGCCGGGGCTGCGGTGCGAGCACTGGCCATGCTGGCTGGGCGGCCAAGCAGCAGCCCTGACTAGGATGACAG  
 CAGCACAAGAGCAACCTTTCTCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTG  
 ATGCACAGCACTGTGCTCCCTATGGGACTCCCTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGCTAC  
 CCCCAGACTGCTGCTTCACTGTATTGAAGAACTGGAGAGGATCTTACGCTCTGCTCTTCCAGGACCTC  
 CAGAAACACAGTGTTCAGAGAGCCCTAAAAAACCTGCTGTCCCAGGACCTATGGTAATGAACACCAACATC  
 TAAACAATCATATGCTAATATGCCATCCTGGAACTCCACTCTGAAGCTCGCCGTTTGGACACCAACACTCCCT  
 TCTCCAGGTCATGACGGATGTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCAGGAAGTC  
 TTTCTGAAGTGTGACCACTTTCTTCTTGTCTGCTTGGGACAGACTCATGCTCTGCTCTGCTTGGCAGAAATGG  
 CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCTAGCTGACCCCTTCACTCTCCCCCTCCCTTTTCTTGT  
 TTTGGGATTAGAAAACCTGCTGTGCAGAGACTGTTATTATTTATTAAAAATATAAGGCTTAAAAAA

**FIGURE 158**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166

><subunit 1 of 1, 761 aa, 1 stop

><MW: 83574, pI: 6.78, NX(S/T): 4

MALPALGLDPWSLLGLFLFQLQLLLPTTTAGGGGQGPMRVRYYAGDERRALSFFHQKGLQ  
DFTDLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMPWPASDRKKSECAFKKKSNETQC  
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTA  
VLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDAFVAAIPSTQVVYFFFE  
ETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL  
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET  
NPRPGSCSVGPSSDKALTFMKDHFMLDEQVVGTPLLVKSQVEYTRLAVETAQGLDGHSHLVM  
YLGTTTGSLLHKAVVSGDSSAHLVEEIQLFDPDEPVRLQLAPTQGAVFVGFSGGVVRVPRAN  
CSVYESCVDCVLARDPHCAWDPEERTCCLLSAPNLNSWKQDMERGNPEWACASGPMSRSLRP  
QSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAPVEASSTVYNGSLLLIVQDGVGG  
LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWP  
HFVTVTVLFAVLVLSGALIIILVASPLRALRARGVKQCETLRPGEKAPLSREQHLQSPKECRT  
SASDVADANNCLGTEVA

**Signal peptide:**

amino acids 1-30

**Transmembrane domains:**

amino acids 136-156, 222-247, 474-490, 685-704



**FIGURE 159**

AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGAAG  
 TGAGC**ATG**GCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCTTCTCCCTGGGGTCTCGCTC  
 TCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGAAGCCATTATCTACTGATGGA  
 CCGGTTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCAACCATGCTTAACCACAAAAGAG  
 GTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCA  
 CCTGAAGATCATCAAAGAGATTAAAAAGAGTTTTGATTTCTTCTGGAAGAACTTTAGG  
 TGGCAGAGGAAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTC  
 ATTTTAAATAGAAAGGATATCATGGATTCTTAAAGAATGAGAAGCTTCGACATGGTGATA  
 GTTGAACTTTTGACTACTGCTCTTCTGATTGCTGAGAAGCTTGGGAAGCCATTGTGGC  
 CATTCTTCCACTTCATTGCGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTCT  
 CAGTATTCGGTTCCTTGTCTGACTGATCACATGGACTTCTGGGCGCAGTGAAGAAATTTCTG  
 ATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTTGACAACACCATCAA  
 GGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGT  
 GGTTCATTAACCTGACTTTGCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTAT  
 GTTGGAGGCTTGATGGAAAAACCTATTAAACAGTACCACAAGACTTGGAGAATTTCTTGC  
 CAAGTTTGGGGACTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTGAGA  
 ATCCGGAATCTTCAAGGAGATGAACAATGCCTTGTCTACCTACCCCAAGGGGTGATATGG  
 AAGTGTCAGTGTTCTCATTTGGCCAAAGATGTCCACCTGGCTGCAAAATGTGAAAATTTGGA  
 CTGGCTTCTCAGAGTGACCTCCTGGCTCACCAAGCATCCGTCTGTTTGTCAACCACGGCG  
 GGCAGAAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCATGGTGGGGATCCCTCTCTTT  
 GGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTATTCAAGTT  
 AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAAACAAATCATGGAAGACAAGAGAT  
 ACAAGTCCGCGGCGAGTGGCTGCCAGTGTCTCCTGCGCTCCCAACCGCTCAGCCCCACACAG  
 CGGCTGGTGGGCTGGATTGACCACGCTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTA  
 TGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTGACGTTTTGTGTTTCTGCTGGGGC  
 TCACTCTGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGGCTGCGT  
 GGGGCCAGAAAGGTGAAGGAGACAT**TA**AGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGG  
 GCGATGTCAACATTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCTCTC  
 TAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGC  
 TAATTTTGCTACAAATTATCCTTACTAGCTCCTGCGTGTAGCAGAAAACTTTCCAGTCTCT  
 CTTGTCTCCTTTGTTTGGCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTG  
 GACCCTGACCTCAGATTTCCAGCCTTAAATCCACCTTCTTCTCATGCGCCTCTCCGAA  
 TACACCTTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCCTCTCAGCTCTCGCCCC  
 TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTCTTTCAAGTTTCTGTTT  
 TGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTCAAGGC  
 CGGACACAGGCTCAGAGGTCTCCACATTGGGTCCCTGTCTCTGGTGGCCACAGTGAGCTCCT  
 TCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAAAATAAAAGTTTACA  
 GCGTTATCTCTCCCAACCTCACTAA

**FIGURE 160**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169
><subunit 1 of 1, 523 aa, 1 stop
><MW: 59581, pI: 8.68, NX(S/T): 1
MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKRGP
FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF
LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPFFVAILSTSFGSLEFGLPIPLSYVPV
FRSLLTDHMDFWGRVKNFLMEFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLKAELEWF
INSDFAFDFAFPLLPNTVYVGGLEKPIKPVQDLENFIAKFGDSGFVLVTLGSMVNTCQNP
EIFKEMNNAFAHLPGQVIWKQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQ
NSIMEAIQHGVPVVGIPVFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK
SAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPYVFQQPWHEQYLFDFVFVFLGLT
LGTLLWLCGKLLGMAVWWLRGARKVKET

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**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 483-504

**FIGURE 161**

GGGCTGTTGATTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT  
GCCTTGGCATATGCACACTACACATTTCTGTACACCCGTCACACACACATACCATGTT  
CTCCATCCCCCAGGTCACGCCCTCAGTGTGTCCCATCCAGCAGGGCTACCTGAAGCTCT  
GGCTGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCTTTCTCTCCAAAGCCCA  
ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGT  
GGGAGCGAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTCAGCCAGCCTAGAGAGGGC  
AGACTATCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAACAGAAGAGGGGCGAGA  
AGACCGGGGCACTTGTGGGTTGCAGAGCCCCCTCAGCCATGTTGGGAGCCAAGCCCACTGGC  
TACCAGGTCCCCTACACAGTCCCGGGCTGCCCTTGGTTCTGGTCTTCTGGCCCTGGGGGCC  
GGGTGGGCCCAGGAGGGGTGAGAGCCCGTCTGTGGAGGGGGAGTGCCCTGGTGGTCTGTGA  
GCCTGGCCGAGCTGCTGCAGGGGGGCCGGGGGAGCAGCCCTGGGAGAGGCAACCCCTGGGC  
GAGTGGCATTGTCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGGC  
ACCAGTGGGGCCATCTACTTCGACCAGGTCTGGTGAACAGGGGCGGTGGCTTTGACCGGGC  
CTCTGGCTCCTTGTAGCCCCGTGCCGGGTGTCTACAGCTTCCGGTTCCATGTGGTGAAGG  
TGTACAACCGCCAAACTGTCCAGGTGAGCCTGATGCTGAACAGCTGGCCTGTCTCTCAGCC  
TTTGCCAATGATCCTGACGTGACCCGGGAGGCGAGCCACCAGCTCTGTGCTACTGCCCTTGA  
CCCTGGGGACCGAGTGTCTCTGCGCCTGCGTGGGGGAATCTACTGGGTGGTTGGAAATACT  
CAAGTTTCTCTGGCTTCTCATCTTCCCTCTCTGAGGACCCCAAGTCTTTCAAGCAAGAAT  
CCAGCCCTGACAACTTTCTTCTGCCCTCTCTTGCCCCAGAAACAGCAGAGGAGGAGAGAG  
ACTCCCTCTGGCTCCTATCCCACCTCTTTGCATGGGACCCGTGTCCAAACACCCAAGTTTAA  
GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAGGCTTTCCACCCACCCACCCCAAGTTACC  
CTCCAGCCACCTGTGTGATCTGTTCTGCCCTGCAGCCCTAGGATCAGGGCAAGGTTTGGCA  
AGAAGGAAGATCTGCACTACTTTGCGGCCCTCTGCTCCTCCGGTTCCCCACCCAGCTTCCT  
GCTCAATGCTGATCAGGACAGGTGGCGCAGGTGAGCCTGACAGGCCCCCACAGGAGCCAG  
ATGGACAAGCCTCAGCGTACCTGACGGCTTCTTCTGTGAGGAAAGCCAGCATCACGGATC  
TCAGCCAGCACCGTCAGAAGCTGAGCCAGCACCGTATAGGGCTAGGGTGGGAGGCTCAGCCAC  
AGGCAGAAGGGTGGGAAGGGCTGGACTCTGTGGTGTAGGAAGGAAGGAGGTGTATTG  
TCTAGACTGAACATGGTACACATTCGCACTGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT  
GGCTGTCTTCTATGCTGGATCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG  
GGTGAGTGTGTTTGTCTGCGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG  
ACCATGGAAGAACATCGATAACCATGCATCCTCTTGTCTGGCCACCTCCTGAAACTGCTCCAC  
CTTTGAAGTTTGAACTTTGTCCCTCCCACTCTGACTGCTGCCCTCTTCTCCAGCTCTC  
TCACTGAGTTTATCTTCACTGTACCTGTTCCAGCATATCCCACTATCTCTTCTCTGAT  
CTGTGCTGTCTTATTCTCTCTTAGGCTTCTTATACCTGGGATTCATGATTCTTCTCTT  
CAGACCTCTCTCTGCCAGTATGCTAAACCTCCCTCTCTCTTCTTATCCGCTGTCCCAT  
GGCCAGCCTGGATGAATCTATCAATAAAACAAGTATAGAAATGGTGGTCACTGAGACACTAT  
AGAATTACTAAGGAGAAGATGCCCTTGAGTGGATGGGTGTACAGGTACAAGTAGGTA  
TGTTCAGAGAGAAATAAATATCAAACGTATATACTAAATTAATAA

**FIGURE 162**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180

><subunit 1 of 1, 205 aa, 1 stop

><MW: 21521, pI: 7.07, NX(S/T): 1

MLGAKPHWLPGLHSPGLPLVLVLLALGAGWAQEGSEPVLLGECELVVCEFGRAAAGGPGGA  
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY  
SFRFHVVVKVYNRQTVQVSLMLNTWPFVISAFANDPDVTREAAATSSVLLPLDPGDRVSLRLRRG  
NLLGGWKYSSFSGFLIFPL

**Signal peptide:**

amino acids 1-32

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**FIGURE 163**

[illegible]

**FIGURE 164**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTIIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLI AVL YFTWLVFDWNTPKKGGRS
QWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAF CNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLREYLMSSGICPVSRDTIDYLLSKNGSGNAIIIVVGAAESLSSM
PGKNAVTLNRKGFVKLALRHGADLVPIYSFGENEVYQVIFEEGSWGRWVQKKFQKYIGFA
PCIFHGRGLFSSDTWGLVPYSPITTVVGEPI TIPKLEHPTQQDIDLYHTMYEALVKLFDK
HKTKEGLPETEVLEVN
```

**Important features of the protein:****Transmembrane domain:**

amino acids 76-97

**N-glycosylation sites.**

amino acids 60-63, 173-176, 228-231

**N-myristoylation sites.**

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

[illegible]

**FIGURE 166**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFVSVVSGLVINQVQLCTLALWPVSKQLYRRRLNCRSLAYSLWSQLV
MLELWWSCTECTLFDTQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFVGLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHK
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGILYGKK
YEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIIYNQKGMFPGEQFKPARRPWTLN
FLSWATILLSPLFSFVLGVFASGSPLLILTFLGFVGAASFGVRRRLIGESLEPGRWRLQ
```

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 307-323, 335-352

**Tyrosine kinase phosphorylation sites.**

amino acids 160-168, 161-169



**FIGURE 167**

GATATTCTTTATTTTAAAGAATCTGAAGTACTATGCATCACTCCCTCCAATGTCCTGGGGCA  
 GCCACCAGGCATATTCATCTTTGTGTGTTTTTCTTTTGCTTTAGCACTGGGGCACTTCTT  
 GCTTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTTGTTGGGTTGGTGGCAGGCAGGCCG  
 GCTTACGCCCTGATACGGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTTATACAAATGGG  
 GATAGCTGGGGTCTGAGACCTGCTTCCTCAGTAAATTCCTGGGATCTGCCTATACCTTCTT  
 TTCTCTAACCTGGCATAACCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTTCTTAGGATCAA  
 AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCCTGCCCCCTGGCCAGCTTCATGT  
 ACATGTGGTGTCTCTTGTGCTTCCTGTAATGTGGTATGCCATGGGGTCTTGCACAAGCCT  
 TTCCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCCTACTTAATATGTAGTC  
 ATCCTGCAGATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT  
 CTTGTTTAATGCTCTCATAAGACCACTTGTTTTCCCTTTTGCAGCACTTGCCACTCAGTTGTA  
 TCTTTATGTGCGTTTGTGGTTGTATGGGTTGTGTCTGTTCCCCAGAATGCCAGCTCTGAGC  
 TGCGTGAGGGTCAAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCT  
 CATGTTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCA  
 GATGGTGTAGGGCCCAGCATTGTAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGA  
 TGCAGGTCCCTGATTACAGTAGGCCCAGGTTGGGCATCTCTAACAACTCCCAGTGATGCTGA  
 TGCTGGTCCATGAACCTATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGC  
 TCACACCTATGATCCAGCACTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT  
 TCAAGACTAGCCTGGCCAACATGGTGGAACCCCATCTGTACTAAAAATACACAAATTAGCTG  
 GGCATGGTGGCACATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG  
 AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGAC  
 AGAGTGAGACTCTATGTCAAAAAAAAAAAAAA

**FIGURE 168**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHHSLQCPGAATRHHLCVCFSFALALGHFLLISLVGKGLSLSCGVGGRQAGRLIRPWVRR
EGKINFYTINGDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSFLGSKYLELQEPSWS
GPCPPGQLHCTCGVLLSFL
```

**Important features of the protein:**

**Signal peptide:**

amino acids 1-28

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**FIGURE 169**

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGA  
 TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTCAGCAACTAAAAAGCCAC  
 AGGAGTTGAACCTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGTCTTACTCTACCTAC  
 ATTAATACTGTTTTTTTGTCTCTTGTAACTAGCCTTTACCTTCCTAACACAGAGGATCTGT  
 CACTGTGGCTCTGGCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGTTTCTACCCAC  
 ACCGTCCCTCGAAGCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTC  
 ACCAACTGTCTCACGTCTGGAGGCACTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTTGSTA  
 GCTGCGGCTTTCAAGGTGGGCCTTGCCCTGGCGTAGAAGGGATTGAACAAGCCGAAGATTT  
 CATAGGCGATGGCTCCCACTGCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGG  
 CCAGGACGGGCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCGCCCAT  
 CTAACCTTTTCATGTCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGG  
 AACCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT  
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 AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCCAG  
 CCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCTCCTTCCCTC  
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 CAATTTAAATCATGTTCTAGTAATGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGT  
 TCAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAA  
 TCCAAACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCGGGGTGTGGTGGCCTGTAATG  
 CCAACATTTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTG  
 GCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGT  
 GTGTGCCCTGATCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT  
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 AAAAAATAAAAAAGAATTATGGTTATTGTAA

**FIGURE 170**

```
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><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA
SPCWPLAGAVPSPPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD
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**Signal peptide:**

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63. 100  
64. 100  
65. 100  
66. 100  
67. 100  
68. 100  
69. 100  
70. 100  
71. 100  
72. 100  
73. 100  
74. 100  
75. 100  
76. 100  
77. 100  
78. 100  
79. 100  
80. 100  
81. 100  
82. 100  
83. 100  
84. 100  
85. 100  
86. 100  
87. 100  
88. 100  
89. 100  
90. 100  
91. 100  
92. 100  
93. 100  
94. 100  
95. 100  
96. 100  
97. 100  
98. 100  
99. 100  
100. 100

**FIGURE 171**

GCGGGCCCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC  
 CCGCCGCCTCCTGCCCGCGCC**ATG**ACCCAGCCGGTGCCCCGGCTCTCCGTGCCCGCCGCGCT  
 GGCCCTGGGCTCAGCCGCACTGGGCGCCGCTTCGCCACTGGCCTCTTCTGGGGAGGCGGT  
 GCCCCCATGGCGAGGCCGGCGAGAGCAGTGCCTGCTTCCCCCGAGGACAGCCGCTGTGG  
 CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC  
 CCTGGAGCAGCCGCAGGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTCTTGCCAACC  
 TGGCGCGGCTCATCCAGGCCAAGAAGGCGCTGGACCTGGGCACCTTCACGGGCTACTCCGCC  
 CTGGCCCTGGCCCTGGCGCTGCCCGCGACGGGCGCGTGGTGACCTGCGAGGTGGACGCGCA  
 GCCCCGGAGCTGGGACGGCCCTGTGGAGGCAGGCCGAGGCGGAGCACAAAGATCGACCTCC  
 GGCTGAAGCCCGCCTTGAGAGCCCTGGACGAGCTGCTGGCGGCGGGCAGGCCGGCACCTTC  
 GACGTGGCCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA  
 GCTGCTGCGACCCGGAGGCATCCTCGCCGTCCTCAGAGTCTGTGGCGCGGGAAGGTGCTGC  
 AACCTCCGAAAGGGGACGTGGCGGCCGAGTGTGTGCGAAACCTAAACGAACGCATCCGGCGG  
 GACGTCAGGGTCTACATCAGCCTCCTGCCCTGGGCGATGGACTCACCTTGGCCTTCAAGAT  
**CTAG**GGCTGGCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCCTGGGAACCCAGGAATTGAC  
 CCTGAGTTTTAAATTCGAAAATAAAGTGGGGCTGGGACACAAAAAAAAAAAAAAAAAAAA

**FIGURE 172**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQVPVRLSVPAALALGSAALGAATGLFLGRRCPPWRGRREQCLLPEDSRLWQYLLSRS
MREHPALRSIRLLTLEQPPQGDSMMTCEQAQLLANLARLIQAKKALDLGTTTGYSALALALAL
PADGRVVTCEVDAQPPPELGRPLWRQAEAEHKIDLRKPALETLDELLAAGEAGTFDVAVVDA
DKENC SAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRYIIS
LLPLGDGLTLAFKI
```

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 8-30, 109-130

**N-glycosylation site.**

amino acids 190-193

**Tyrosine kinase phosphorylation site.**

amino acids 238-246

**N-myristoylation sites.**

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

**Amidation sites.**

amino acids 31-34, 39-42

**FIGURE 173**

[illegible]

**FIGURE 174**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286

><subunit 1 of 1, 671 aa, 1 stop

><MW: 74317, pI: 7.61, NX(S/T): 0

MPHAFKPGDLVFAKMGYPHWPARIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFPYD  
KCKDKYGKPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDEDERG  
VMAVTAVTATAASDRMESDSDSKSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPSE  
EENSESSSESEKTSQDQFTPEKKAARAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPV  
AMARSASSSSSSSSSDSDSVVKKPGRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEV  
DRISEWKRREARRELEARRRREQEEELRRLREQEKEEKERRRERADRGAEERGSGGSSGD  
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEREAKKSAKKPQSSSTEPARKPGQKEKRV  
RPEEKQQAQPVKVERTRKRSEGFMSDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC  
LNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKIEAV  
QKVNKAGMEKEKAEKLAGEEELAGEEAPQEKAEDKPSTDLAPVNGEATSQKGESAEDEKEHE  
EGRDSEEGPRCGSSEDLHDSVREGPDLDPRGSDRQERERARGDSEALDEES

**Signal peptide:**

amino acids 1-13



**FIGURE 175**

GTTGGTTCCTCGGATCTTCACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAATTA  
 ACACCATTTGAAGAGAACATTTGTTTCATC**TAG**GAATGCTAATAAGATGAAGACTTAAAGCCAGAGGCCAAGA  
 TTTTCACTTTTCTGCTTTTGATGATGCTAAGCATGACCATGTTGTTCTCCAGTCACTGGCACTTTGAAGCA  
 AAATATTCCAAGACTCAAGCTTAACCTACAAAGACTTGTGCTTTCAAATAGCTGTATTCCTTTTGGGTTTCATC  
 AGAAGGACTTGGATTTCAAACCTCTTCTTTAGATGAGGAAAGAGGCAGGCTGCTCTTGGGAGCCAAAGACACAT  
 CTTTCTACTCAGTCTGGTTGACTTAAACAAAAATTTAAGAAATTTATTGGCCTGCTGCAAGAGAACGGGTGGA  
 ATTTATGTAAATTAGCTGGGAAGATGGCAATACAGAATGTGCAAATTTATCAGAGTACTTCAGCCCTATAACAA  
 AACTCACATATATGTGTGGAACTGGAGCATTTCATCCAATATGTGGGTATATTGATCTTGGAGTCTCAAGGA  
 GGATATTATATTCAAACTAGACACACATAATTTGGAGTCTGGCAGACTGAAATGTCCTTTGCATCCTCAGCAGCC  
 TTTTGCTTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCCCTTGGCAAGATACCTGCAAT  
 CACTCGATCCCTTGGGCTACTCATGACCACCACTACATCAGAAGTGCATTTAGAGCACTACTGGCTCAATGG  
 AGCAAAATTTATTGGAACTTTCTTCATACCAGACACCTACAATCCAGATGATGATAAAATATATTCTCTTTTCG  
 TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCCTCTTCTCGAGTTGGAAAGAGTTTGTAAAGATGATGT  
 AGGAGGACACAGCAGCTGTATAAACAGTGGACGACTTTTCTTAAGGCCAGACTGATTTGCTCAATTCCTGGAAG  
 TGATGGGCGAGATACTTACTTTGATGAGCTTCAAGATATTTATTACTCCCCAACAGAGATGAAAGAAATCCTGT  
 AGTATATGGAGCTTTACTACAACAGCTCCATCTTCAAAGGCTCTGCTGTTTGTGTATAGCATGGCTGACAT  
 CAGAGCAGTTTAAATGGTCCATATGCTCATAGGAAGTGCAGACCATGTTGGGTGCAGTATGATGGGAGAT  
 TCCCTTTCCACGGCTCGGTACATGTCCTCAAGCAAAACCTATGACCACTGATTAAAGTCCACCCGAGATTTTCCAGA  
 TGATGTCATCAATCTTATAAGCGCAGCTCTGTGATGATAAGTCGTATACCCAGTTTCGAGGAGGCCACAGCTT  
 CAAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCATGCTTTGCAGAGATGGCCAGTACGA  
 TGTAAATGTTCTTGGACACAGACTTGGAACTGTCTCAAAGTTGTGCAGCATTTCARAAGAAAAGTGGAAATATGGA  
 AGAGGTAGTGTGGAGGAGTTGCAGATATTCAGCACTCATCAATCATCTTGAACATGGAATTTGTCTGTGAAGCA  
 GCAACAATGTACATTTGGTCCGAGATGGATTAGTTGAGCTCTCTTTCGACAGATGAGCACTATTGGGAAAGC  
 TTGCGCAGACTGTGTCTTGGCAGAGACCCCTACTGTGCTGGGATGGAATGATGCTCTCGATATGCTCCCTAC  
 TTCTTAAAGGAGGAGCTAGAGCCGCAAGATGTAAATATGGCGACCAATCACCAGTGTCTGGGACATCGAAGACAG  
 CATTAGTCATGAAATCTGTGATGAAAAGTGATTTTGGCATTGAATTTAACTCAACCTTTCTGGAATGTATACC  
 TAAATCCCAACAGCAACTTTAAATGGTATATCCAGAGGTCAAGGGATGAGCATCGAGAGGAGTTGAAGCCCGCA  
 TGAAGAATCATCAAACCGAATATGGGCTACTGATTGGAAGTTTGCAGAAGAAGGATTCTGGGATGTATTACTG  
 CAAAGCCGAGGAGCACACTTTCATCCACCCATAGTGAAGCTGACTTTGAATGTCTTGAATGAACAGATGGA  
 AAATACCCAGAGGGCGAGCATGAGGAGGGCGAGGTCAAGGATCTATTGGCTGAGTCAGGTTTGAGATACAAAGA  
 CTACATCCAAATCCTTAGCAGCCCAAACTTCAGCCTCGACCATGCTGCGAAGCAGATGTGGCAGAGGGAAGGCG  
 GAGACAGAGAAACAGGGGGGCCCAAAGTGGAAAGCACATGCAGGAATGAAGAAGAAACGAAATCGAAGACATCA  
 CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCAG**TAG**TTTTCTACTTAATTTAAAGAAAAGAAATTCCTTACC  
 TATAAAAACATTGCCTCTGTTTTGTATATCCCTTATAGTAATTCATAAATGCTCCCATGGGATTTTGTCAAGG  
 CACAAGACAAATATCTGAATAAGACAATATGTGATGAATATAAGAAAGGGCAAAAATTCATTGTAACAGATTTT  
 CCAAGAACAAATCTTGCACAAGCAAAGTATAAGAAATATCCTAAAAATAGGGGGTTTACAGTTGTAAATGTTT  
 TGTGTTTGAATTTGGAATTTATTGTCATGTAATAGTTGAGCTAAGCAAGCCCGAATTTGATAGTGATTAAGGT  
 GCTTTATCCCTCGAATGTCATTAAAGCATGGAATTTACCATGCACTTGTGCTATGTTCTTATGACAGATATAT  
 CATTCCTTATGAGAACAGCAGTACCTTTGGTAGGGAATAAGAGGTGAGACACAAATTAAGACAACCTCCCATATC  
 AACAGAAATTTCTCAGTGAGCCCTCACTCCTGGAGAAATGGTATAGGAATTTGGAGAGGTGCAATATTTCTTTC  
 TGGCCACTGGGTTAAATTTAGTGACTACACAATGATTTACTGAAGGGCAGTAAATGTTTCCCCAGGATTTCT  
 TGGCATGTGAGGATACAGGTTACAGAGAGAAAGTTGGTGTAGTTAGTTGTTTTAGAGTATATACTAA  
 GCTCTACAGGACAGAAATGCTTATAAATACTTTAATAAGATATGGGAAAATTTTATAAACAAGGAACAACA  
 TAATGATATAATGCATCCTGATGGGAAGGCATCAGATGGGATTTGTAGAAGACAGAAAGGAAGCAGCCAT  
 AAATTTGCTGCTTTGGGAAAACATCATCCCATGAAAGGAAGAACAAATCACAATAAAGTGAGAGATTAATGTA  
 TGAGCTCTTTTCACTAGGTTATAAGTAGCTGCCAATTTGTAATCTGCTGTAAAAAATATCAGATTATAACA  
 AACTGCTAGCAAAATCTGAGGAACACATAAATCTTCTGAAGAATCATAGGAAGAGTAGACATTTTATTATAAAC  
 AATGATATTTAGTATATATTTCTCTTTTAAAAAATATTATCATCATCTGTATATATTTCCTTTTACTGCT  
 CTTTATTTCTCCTGATATTTGGATTTGTGATTATATTTGAGTGAATAGGAGAAACAAATATATACACACAGA  
 GAATTAAGAAATGACATTTCTGGGAGTGGGATATATTTGTTGAATACAGACAGGTGTAAATTTTAACT  
 AACGGAAAGGGTTAAATTAACCTTTTGACATCTTCACTCAACCTTTTCTCATGCTGTGAGTTAACTCTGTGAAT  
 GTAGTATTGTTTTGTAATTTAAACAATAAATAGCCTGCTACATGT

**FIGURE 176**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPLRLKLTyKDLLLSNSCIPFL
GSSEGLDFQTLILLDEERGRLLLGAKDHI FLLSLVDLNKNFKKIYWPAKERVERELCKLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRCLKCPFD
PQQPFASVMTDEYLYSGTASDFLGKDTAFTRS LGPTHDDHHYI RTDISEHYWLN GAKFIGTFF
IPDTYNPDDDKIYFFRESSQEGSTSDKTI LSRVGRVCKNDVGGQ RSLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTTSSIFKGSAVCVYSMADIRAVFNGP
YAHKESADHRWVQYDGRIPYPRPGT CPSKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPV
AGGPTFKRINVDYRLTQIVVDH VIAEDGQYDVMFLGTDIGTVLKVVSISKEKWNMEEVLEE
LQIFKHSSIIILNMLS LKQQQLYIGSRDGLVQLSLHRCDTYGKACADCC LARDPYCAWDGNA
CSRYAPT SKRRARRQDVKYGDPITQCWDIEDSISHETADEKVI FGIEFNSTFLECIPKSQQA
TIKWIYIQRSGDEHREELKPDERI IKTEYGLLIRSLQKKDSGMYCKAQEHTFIHTIVKLTLN
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRQRN
KGGPKWKHMQEMKKKRNRHRLDELPRAVAT
```

**Important features of the protein:****Signal peptide:**

amino acids 1-36

**N-glycosylation sites.**

amino acids 139-142, 607-610, 724-727

**Tyrosine kinase phosphorylation site.**

amino acids 571-576

**Gram-positive cocci surface proteins 'anchoring' hexapeptide.**

amino acids 32-37

**FIGURE 177**

CCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGAGAGGTCATCCTGGAGCATGCCACCOCGGGGAGCAGA  
 CACCTCCCAAGTTAAGCTGGGAGCAAGACCTGAAGCTGTTCTTCAGGAGCCTGGTGATTTTCCCCACCCAC  
 CTCAGACGTTTCAGCCAGCAGGACCTGATCAGGTGTGTCTCTGGAGTGGGAGCAGAAGCGCGCTGGCTGGCAAGA  
 GTGGCCTGGGAGAAAGAGGTTTCAGCGCTTGACAGCCGAGCTGCCCGTGACTACAGATCCAGAACCATGGGCATC  
 GGGTGAGGTTGGGGGGCAGAGGTTGTCATGTGCACCTTCTTGCTCAGCAAGAGAGAGCTGAGAGAGGGGATCTTTGG  
 AGCCATTGAGGGTGTCTATGAGAGTCAGAGGGGGAGGAAAGGTATTTTAAGGTAAACGATGTGCACAAATAGTTAA  
 GAGCACAGTTTTCAGAGCTAGACCAGCATAGGTTCAAATTCCTCTGTTGTCCTAGTTTCTGTAGCCCCAGCT  
 AAGGGAGTGACTTAACTCTCTGGAATCTCAATTTCTCATCACTAAAGTAGGGCCAAATATAGCACCCCACTCAT  
 GGGGAAGATTAAATGACATAATGTATGTG**ATG**CAACTAGCAAAAGTACCAGTCCCATATAGTCTCATGCCCCACAG  
 TATTTCCACCCACCCTGTTCTCTGCTTCCCAACAGGTAAGTGCACACCATGGAGCAGAGGGCGCAGCAGGCTCT  
 CAGAGCGGGAGGCTCCAGCATAGAACAGAGGTTACAGGAAGTGGAGAGAGCATCCCGCCGGCCACAGTGTAGCC  
 AGGTGAAGGGGGCTGCCCGCTGCCCTGCTGACAGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGSCA  
 TGACCCAGGCCAGGATGAGGTGGAGCAGGAGCGCGCTCAGTGGGCTCCGCTCTCCACAGGAGACCTCTCTC  
 CAACCGCTGAGGATGCTGAGCTTCTGACTTTGAGGAATGTAGAGAGACGGGAGAGCTCTTTGAGGAGCTGCC  
 CCCAAGCCCTGGCCACGAGGCCCTCCCTGCCCTGCACAGTGGTATTTCCGATCAGGCGAGGCTGGAGATG  
 AGCTGACAATCCAGGAGGTTGAGTGCCTGGAGGTCATAGAGGAGGAGATGCTGACAGTACAGCCAGGACAGA  
 ACCAGCACGCCGAGTACGCTTTGCTCCCTGAGCGATATCTCAACTTCCCGAGCTCTCCCTCCAGAGAGCAGCC  
 AAGACAGTGACAATCCCTCGGGGCGAGGCCACAGCAATCTTGGCAGAGGCCCTGTACAGCTACACCGGACAGA  
 GTGCAGAGGAGCTGAGCTTCCCTGAGGGGCACTCATCCGTCTGTCGCCCGGGGCCAAGATGAGTAGATGAGG  
 GCTTCTGGAGGGGAGAAATTTGGGGGCGTGTGGGGTCTTCCCTCCGCTGCTGGGAAGAGCTGCTTGGCCCC  
 CAGGGGCCACTGAACCTCTGACCCCTGAACAGATGCTGCCGTGCCCTTCTCTCCAGCTTCTCCCCACTGCAC  
 CTACCTCTGTGTTGGTGGGGCCCTGCACCTGTCTGCTGCCGAGGAGCAAGGCTGGACTTCCCTGGGTTCTCTGG  
 ACATGAGTGCACTCGACTCAGGCGGATGCGTCCACACCTCCCGCGCGGCTAAAGCCCCGGATCTGGGCCACC  
 CAGATCCCCCTCAG**AG**AGGCCAGGGAAGCTTGACCCCCAGTGATGCTGCTGCCCTATCTCAAGCTGTGAGA  
 CCACACCATCAATGATCCAGAGCAACAGCAGCAAAAGCTGGAATCGCCCTTATTTCCACCCCTCAGCTCCAGGGT  
 GGAACCTGCCCTTCCCTATTTCTAGAGCTGGAACCCACTCTTTTTTCCCAATTTGTCATCATCTCTAGGACC  
 GGAATCTACTACCTTCTCTCTGTCATGACCTATCTAGGGTGGTGAATGCTGAAATCTCTGGGGCTGGAAAC  
 ATCCATCAAGGTCTCTAGTAGTCTGCGCCACCTCTTCCCAACCTGGCTCCATGACCCACCCACTCTGGATG  
 CCAGGGTCACTGGGTTGGGCTGGGAGAGGAACAGGCCCTTGGGAATCAGGAGCTGGAGCCAGGATGCGAGCAG  
 CTGTAATGGTCTGAGCGGATTTATGTACAATGAATAAAGGGCAGCAAGGCCAGGCCAGGGCTGGGGCTTTGTG  
 CTAAGAGGGCAGGGGGCTACGGTGCTATTGCTTTAGGGGCCACACAGGGCAGGGGCTGCTCCAGCTGCCAC  
 GCTCTATCATATGGAGCAGGTGTTGGGGAAGGCGGGGCAGGCAGCTTTGCGAGGCAGGGGAAGGAGAGAGAC  
 TGAGGGGCTGTGACCTCTCTGAGGCCCCAGCCTGAGACTGTGCAACTCCAGGTGGAAGTAGAGCTGTTCCCTC  
 AGCTGGGGGGCAGTGCTGCTCAAGTGGAGGGGAGGGCTTTCACGCCACCCACCCCTGGCCCTGCCAGCTGGTAG  
 TCCATCAGCAATGAAGGAGACTTGGAGAGAGGAAGAATAACACTGTGCTTCTCTCAAGCTGTGTGTCAGC  
 TTTTCCCTGGGGCTCCAGGACCTTCCCTACCTCCACCAACCAAGAGCACTTATGACAAAGGCTTAAGCCTGC  
 AGTTTACTCTGGGGTTCAGGAGCGCAAGAGCTTAATAGTTTAAGTAGTGATGGGAAGATGAGATTAACCTCA  
 TTTAGGGCTCAGGAGCACTCACTCATATACTCCTGCTCCCTGTGGTAGAGCACTGAGAGAAAGGGGAGGGG  
 TCAACAAATGAGAGCCAGGAGTAGTCTATCAGTGCCCCCAGAGTAGAGAGCAATAAGAGCCGCCAGCCAGTGG  
 AGTCCCGGCTGTGTTTTCCTACCTGGTGATCAGAAGTGTCTGGTTGCTTGGCTGCCATTTGCTCTGTAGTGG  
 CAGGCCCTGGGCTTGGGCCCTCCCTCCGGCCCTCAGTGTGGCTCTGCAGAGCTCTGGGTTCCGCTCAAGTG  
 CAGAGGGGTTAGGCTGCTGCTCCGTAGCTCCTCCATCTGACTGGGGGCTGGCTAGAGCTGGGGCTGGGCTGCC  
 TCTCAGGGGACGCTCTCCATGCCAGGCATCCCTGCCCTTGGCTGCCCTCCCGACACCCCTGACCACCCCTG  
 GGTCCCTGCCCCACAGAGCCCAAGCTCCTGCTGCTGGGGAGCCATCAGGTGTTCTGTCAGTCTCATAGGCT  
 TCTCAATGTGTGTCACCCGGAACCTGGGAGGGGAGGAACTGGGTTTAGGACACACATCAGAGGCTGCTGTG  
 GCCCTCCCTCTGACCAAGGACATCTGAGTTTGGTGGCTACTTCCCTCTGGCTAAGTAGGGGAGGCGCTCTCT  
 AGATTGTGGGGAGCAATGTGAGCTGACTTCTGCTGGAGCTCCCGATCCAGAGGAAGAGGAGGCCCACTT  
 TGGGATCAGTGCCATCATCACTGGGCCCTTACCTCAGCTAGCCCTTCTCCTGGAGCAGCTGCCCACTGCCCA  
 CAGAGCAACAGTGGTCTCCCTGTCGGGGGCGGCTTTTCTGCTGGAGCTCCCTGACGAGCAAGTGGAG  
 GCTCTTCTGCTGCGCTGCAATGGATGCAAGGGGCTCAGAGCCAGGTGCACTGTGTGATGATGGAGGGGGCTC  
 GCTCCTGCGGCTGGAGGTGGCATCCACATGGACAGGAGGGGGGATGAGGTAAGCAATTTCCATTTCCCT  
 TCAATGTTTGTCTTACGTTCTTTCAGCATGCTCCTTAAACCCCAAGAGCCCAATTTCCCAAGGCCCAATTT  
 TTTCTGTCTTATCTAATAAATCAATTAAG

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA
QVSQVKGAAARLALLQGAGLDVERWLKPMTAQQAQDEVEQERRLSEARLSQRDLSPTAEDAELS
DFEECEETGELFEPPAQALATRALPCPAHVVFYRQAGREDELITITEGWLEVIEEGDADEW
VKARNQHGEVGVFPERYLNFPDLSLPESSQSDNPNCGAEPTAFLAQAALYSYTGQSAEELSFP
EGALIRLLPRAQDGVDDGFWRGEGFGRGVVFPSLLVEELLGPPGPPELSDEQMPLSPSPSPS
FSPAPTSLVDGPPAPVLPGDKALDFPGFLDMMAPRLRPMRPPPPPAKAPDPGHDPDLT
```

**FIGURE 179A**

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGAGGAAAGAGACAGAGACAAAGGCCACAGCGGAA  
 GAAGGCAGAGACAGGGCAGGCACAGAAAGCGGCCACAGACAGAGTCTTACAGAGGGAGAGGCCACAGAGAGCTGCAGA  
 AGACACAGGCGAGGGAGACAAAGATCCAGGAAGAGAGGGCTCAGGAGGAGATTTGGAGAGAGCCAGACCCTGG  
 GCACCTCTCCCAGGCCAGGAGCTAAGTTTCTCTCATTTCTCTTAACGGCTCCTCAGCCCTTCTGAAACTTTGCC  
 TCTGACCTTTGGCAGGATCCAAAGCCCCAGGCTACAGAGAGGAGCTTTCCAAAGCTAGGGTGTGGAGGACTTGGT  
 GCCTTAGACGGCTCATCTCCTCCAGCTGCAGTACCAGTGGCAGTCCAGAGCAGGGCTGCATCTCCGGGAGGG  
 CTTCGACGGGCTGGCTGTGGGGGAGCCAAACCTTGCCTCTGCTCCCAATTTGCGGCTCTCTGGCTGTGCTGG  
 GTGCTTCTGCTACTGTGGCTCTCTCTGCTCCTCAGCCCGCTGGCAGGCCCTCCCGGGGAGGAGAGAT  
 CGTGTTCAGAGAGCTCAACGGCAGGCTCTGCTGGCTGGCTGGGCGCCCTGCCAGGCTGTTGTGCGCTTGC  
 GGCCTTTGGGAGACGCTGCTACTAGAGCTGGAGCGGACTCCGCTGTGCAGTTCGAGGGCTGCAGTGCAGTA  
 CTTGGGCCAGGCGCTGAGCTGTGGGTGGAGCAGAGCCTGECACCTACCTGACTGGACCATCAATGAGATCC  
 GGAGTCGTGGCTCTCTGCAGTGGGATGGGGAGCCCTGTTAGGCTGTTACAATATCGGGGGCTGAACCTCCA  
 CTTCCAGCCCTGGAGGGAGGACCCCTAACTCTGCTGGGGACCTGGGGCTCACATCTACGCGGAAGAGTCC  
 TGCAGCGGTCAAGTCCCATGTGCAACGTCAAGGCTCTCTTGGAAAGCCCAAGCCCAAGCCCCAAGAGCCAA  
 GCGCTTTGCTTCACTGAGTAGATTGTGGAGACACTGGTGGTGGCAGATGACAGATGGCGCATTCACCGGTGC  
 GGGGCTAAAGCGCTACCTGCTAACAGTGATGGCAGCAGCAGCCAGGCTTCAAGCACCCAAAGCATTCGCAATCC  
 TGTACGTTGGTGATCTGGCTAGTGTATCCTGGGCTCAGGCGAGGAGGGGCCCAAGTGGGCGGAGTGTCTGC  
 CAGACCTCCGCGCATCTTGTCTGGCTGGAGCGGGGCTCAACACCTTGAGGACTTCGGGCTGACCACTTTGA  
 CACAGCCATTCGTTTATCCGCTCAGGACCTGTGTGAGTCTCCACTTGGCACACGCTGGGCTATGGCTGATGTGG  
 CACCGTCTGTGACCGGCTCGGAGCTGTGCCATTGTGGAGGATGAGGGCTCAGTCAAGCTCTACTGCTCTCA  
 TGAATGGGTCATGCTTTCAACATGCTCCATGACAACCTCAAGCCATGCATGAGTTGAATGGGCTTTGAGAC  
 CTTCCGCTGATGCTGGCCGCTGTGATGGCTCATGTGATCTTGGAGGAGCCCTGAGTTCGAGTCCCGGCTT  
 CATCATCTGATCTTCTGGACAAATGGCTATGGGCACTGTCTTATAGACAAACAGAGGCTCATGATGCTGCTGT  
 GACTTTCCCTGGCAGGACTATGATGCTGACCGCAGTGGCAGCTGACTTCGGGCGGAGTCAAGGCTATTGCC  
 ACAGCTTCGCGCGCCCTGTGCTGCTCTGTGCTCTGGCAGCTCAATGGAGCATGCCATGCGACAGCAAAACA  
 CTCGCCCTGGGCGATGGCACAACCTCGGGGCGCAGAGGCTCAGTGGGTGGTGCCTGCTCCCATGAGCCA  
 GCTCCAGGACTTCAATATTTCAAGGCTGGTGGCTGGGCTCCTTGGGAGCACTGGGCTGACTGCTCTCGGACCTG  
 TGGGGTGGTGTCCAGTTCTCTCCGAGACTGCACAGGCGCTGTCCCGGAAATGGTGGCAAGTACTGTGAGGG  
 CGCGGTAACCGCTTCGCTCCTGCAACACTGAGGACTGCCAACTGGCTCAGCCCTGACCTTCGCGAGGAGCA  
 GTGTGCTGCTTACAACACCGCACGCACTCTTCAAGAGCTTCCAGGGCCCATGGATGGGTTCTCGCTACAC  
 AGCGTGGCCCCCAGGACAGTGCAAACTCACTGCCAGGCCCGGGCACTGGCTACTACTATGTGCTGGAGCC  
 ACGGTTGGTAGATGGGACCCCTGTTTCCCGGACAGCTCCTCGGTCTGTGTCCAGGGCCGATGCATCATCTGG  
 CTGTGATCGCATTTGGCTCCAAAGAAAGTTTGAACAGTGCATGGTGTGGGAGGGGACGGTTCTGGTTGCA  
 CAGAGCAGTCAAGGCTCTTCAGGAAATTCAGGTACGGATACAACAAATGTGGTCACTATCCCGCGGGGCGCACCA  
 CATTTCTGTCCGCGAGCAGGGAACCTGGCCACCGGAGCATTACTTGGCCCTGAAGCTGCCAGATGGCTCCTTA  
 TGCCTCAATGGTGAATACAGCTGATGCCCTCCCCACAGATGTGGTACTGCTGGGCACTGAGCTTGTGCTA  
 CAGCGGGGCACTGCAGCTCAGAGACACTGTCAAGGCTGGGCACTGGCCAGGCTTGAACATGCAAGTCTCT  
 AGTGGCTGGCAACCCCCAGGACACAGCTCCGATACAGCTTCTCTGTCGCCCGGCCACCTTCAACGCCACG  
 CCCCCTCCCCAGGACTGGCTGCACCGAAGAGCAGATTTCTGGAGATCCTTCGGCGCGGCCCTGGCGGGCAG  
 GAAATTAACCTCATATCCCGCTGCCCTTTCTGGGCACCGGGGCTCGGACTAGTCTGGGAGAAAGAGAGACTT  
 CTGTTGCTGCTCATGCTAAGACTCAGTGGGAGGGGCTGTGGGCGTGAGACTTGCCTCTCTGCTCAAT  
 GCGGAGCTGGCCCTGCGCTGCTTCTGCTGCGCTGGGAGGACAGTGGTGTAGTGATGGAAGGGCTCAGACAG  
 AGCCCTGCATCAATACTGCCCTCTGCGCTCGGGTCAACAGGAGGAGGGGGAAGGACAGGAGGGCTTGGGCC  
 CAGTTGCTATTTATTTAGTATTTATTTCACTTTTATTTAGCACAGGGAAGGGAAGGACTAGGTTCTGTGGGAA  
 CTTGACCCCTGACCCCTCATAGGCTCACCCTGGGCTAGGAAATCAAGGTTGGTGGTATAGGTATTAAGTGGT  
 TGTGTATGCTGT  
 TTTCTTGAATTTTATTTTGGGAAAGAAAAGTCAAGGATAGGTTGGGCTTCAAGGAGTGAAGGATATCTTTT  
 TTTTTTTCTT  
 GCAACATCTCGGCTCAGTGCATCTTCGCGCTCCCGGTTCAAGTATTTCTCATGCTCAGCTCTTCTGCTGATG  
 GGATACAGGCTCTGCGACAGCAGCCAGCTAATTTTGTGTTTGTGTTGGAGACAGATCTCTGCTATTTGTCT  
 ACCAGGCTGGATGATTTTCACTCAGTCAACCTTCGCCACCTGGGTTGCCAATCTCTCGCTCAGCTCC  
 CAGTAGCTGAGTATATAGGCACTTACCACACGCGCGCTAATTTTGTATTTTATGACAGAGGCTTTTAC  
 CATGTTGGCAGGCTGTGCTGCACTCTGACCTTATGATGATCCTGCTCTCATCTCCCAAGGCTTGGGAT  
 ACAGGCTGAGCACCGCTGCTGGCCAGCCCACTAATTTTGTATTTTATGACAGAGGCTTTCAACATCT  
 TGGCAGGCTGCTCTTGAATCTGACCTCAGGTAATCGACTGCTCGGCTCCCAAGTGTCTGGGATTACAG  
 TGTGAGCCACACGCGCGGTACATATTTTAAATTTGAATTTACTATTTATGTGATCCTTTTGGAGTCAGACG

**FIGURE 179B**

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**FIGURE 180**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRLAGRWLWGAQPCLLLPVPLSWLVWLLLLLLASLLPSARLASPLPREEEIV  
FPEKLNQSVLPQSGAPARLLCRLQAQFGETLLLELEQDSGVQVEGLTVQYLGAPELLGGAEF  
GYLTGTGIDPESVASLHWDDGALLGVLYRGAEHLQPLEGGTPNSAGGPGAHILRRKSP  
ASGQGPNCNVKAPLQSPSPRRRAKRFASLSRFVETLVVADDKMAAFHAGLKKRYLLTVMAA  
AAKAFKHPSIRNPVSLVTVRLVILGSGEEGPQVGPSSAAQTLRSFCAWQRLNTPEDSGPDHF  
DTAILFTRQDLCGVSTCDTLGMADVGTVCDFPARSCAIVEDDGLQSAFTAHELGHVFNMLHD  
NSKPCISLNGPLSTSRHVMAPVMAHVDPEEFWSPCSARFITDFLDNGYGHCLLDKPEAPLHL  
PVTFFPGKDYDADRQCQLTFGPDSRHCPQLPPPCAALWCSSGHLNGHAMCQTKHSPWADGTFPCG  
PAQACMGGRCLHMDQLQDFNIPQAGGWGFWGFWGDCSRTCGGGVQFSSRDCTRPVPRNGGKY  
CEGRRTFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPQPMQVPRYTGVAPQDQCK  
LTCQARALGYYYVLEPRVVDGTPCSPDSSSVQVQGRCIHAGCDRIIGSKKFFDKCMVCGGDG  
SGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQGGNPGHRSIYLALKLPDGSYALNGEYTL  
MPSPTDVVLPGAIVSLRYSGATAASETLSGHGFLAQLTLTQVLVAGNPQDTRLRYSFVFRPT  
PSTPRPTQDWLHRRQAILEILRRRPWAGRK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-48

**N-glycosylation site.**

amino acids 68-71

**Glycosaminoglycan attachment site**

amino acids 188-191, 772-775

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 182-185

**Tyrosine kinase phosphorylation site.**

amino acids 730-736

**N-myristoylation sites.**

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-  
172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-  
582, 679-684, 682-687, 763-768

**Amidation sites.**

amino acids 560-563, 834-837

**Leucine zipper pattern.**

amino acids 17-38, 24-45

**Neutral zinc metalloproteinases, zinc-binding region signature.**

amino acids 358-367

**FIGURE 181**

CAGCAGTGGTCTCTCAGTCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACC**ATGG**  
 CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCC  
 AAGAAAAATGTAAATCACTTAAGATTTGTGGACTGGTGTGTTGGTATCCTGGCCCTAACTCT  
 AATTGTCTCTGTTTTGGGGGAGCAAGCACTTCTGGCCGAGGTACCCAAAAAGCCTATGACA  
 TGGAGCACACTTCTACAGCAATGGAGAGAAGAAGAAGATTACATGGAAATTGATCCTGTG  
 ACCAGAAGTGAATATTCAGAAGCGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT  
 TAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGA  
 TTAAAGTGATTCTGAATTTCTGAACCAGAGAGGAAATAGATGAGAATGAAGAAATTACC  
 ACAACTTTCTTTGAACAGTCAGTGATTGTTGGGTCCAGCAGAAAAGCCTATTGAAAACCGAGA  
 TTTTCTTAAAAATTCCAAAATTCTGGAGATTGTGATAACGTGACCATGTATGGATCAATC  
 CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTT  
 CCTGCCAACGAAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAGT  
 AGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGAAGAAGTTCATAAATGACTATACTG  
 AAAATGGAATAGAAATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGT  
 CGAGGCAACCGCTATTGCCGCCGCTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA  
 CTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATGCCCTGTAACTGGTGGGTGGCCC  
 GCATGCTGGGAGGGTCT**TAA**TAGGAGGTTTGAGCTCAAATGCTTAACTGCTGGCAACATAT  
 AATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCCGGTAGCCAGCT  
 CTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC  
 AAAAAAAAAAAAAAAAAA



**FIGURE 182**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHIINAEAFKSKKICKSLKICGLVFGILALTILVLFWGSKHFWEVPPKAY
DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSNGTDETLVHDFKNGYTGIFYVGLQKCFIKT
QIKVIPEFSEPEEEIDENEEITTTFFEQSVIWPVPAEKPIENRDFLKNKILEICDNVTMYWI
NPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEELPINDY
TENGIEFDPMLDERGYCCICYRRGNRYCRRVCEPLLGYYPYCYQGGRVICRVIMPCNWWW
ARMLGRV
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**Important features of the protein:****Signal peptide:**

amino acids 1-40

**Transmembrane domain:**

amino acids 25-47 (type II)

**N-glycosylation sites.**

amino acids 94-97, 180-183

**Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

**N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 315-317

**Cytochrome c family heme-binding site signature.**

amino acids 9-14

**FIGURE 183**

GCGGAAC TGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCGAGGGCCCAGGGAGCTGCC  
 CGGCTGGCCTAGGCAGGCAGCCGCACC**ATG**GCCAGCACGGCCGTGCAGCTTCTGGGCTTCCT  
 GCTCAGCTTCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGA  
 CAGCGCACGTGGGCACCAACATCCTCAGGGCCGTGTCTACCTGAAAGGGCTCTGGATGGAG  
 TGTGTGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCC  
 CCAAGACCTCCAGGCTGCCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCT  
 GCGCCTGCGCCGTATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCCGCCAAGACC  
 ACCTTTGCCATCCTCGGCGGCACCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGT  
 CTCCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCAGCGGCATGA  
 AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATGGT  
 GGCACCCTGCTTTGCCTGTCTGCCAGGACGAGGCACCCTACAGGCCCTACCAGGCCCCGCC  
 CAGGGCCACCACGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG  
 ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG  
**TGAG**TCCCCACAGCCTGCTTCTCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTC  
 AATGGAGGCAGGGGTTCCAGCACAAAGTTTACTTCTGGGCAATTTTGTATCCAAGGAAATA  
 ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGAAATAAGAGGAGGAGAA  
 AGCTCTCTATACCAAGACTGAAAAAAAAAATCCTGTCTGTTTTTGTATTTATTATATATAT  
 TTATGTGGGTGATTTGATAACAAGTTTAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGT  
 TGGTTTGTGATCCAGGAATAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAAA

**FIGURE 184**

MASTAVQLLGFLLSFLGMVGTLLITLPHWRRTAHVGTNILTAVSYLKGLWMECVVHSTGIY  
 QCQIYRSLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAGTPAKTTFAILGGTL  
 FILAGLLCMVAVSWTTNDVVQNFYNPLPSGMKFEIGQALYLGFISSSLIGGTLCLSCQ  
 DEAPYRFPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domains:**

amino acids 82-103, 115-141, 160-182

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**FIGURE 185**

GAGCTCCCCCTCAGGAGCGGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCG  
 CAGGCGGCAGGGCGGGCGGCCAGGAT**CATG**TCACCACCACATGCCAAGTGGTGGCGTTCCCT  
 CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGATGGACATGTGGAGCACCC  
 AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC  
 GTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCCTATTTACCATCCTGGGACTTCCAGC  
 CATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCTGGGTGCCATTGGCCCTCC  
 TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC  
 AACATGACACTGACCTCCGGGATCATGTTTCATTGTCTCAGGTCTTTGTGCAATTGCTGGAGT  
 GTCTGTGTTTGCACACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCG  
 GCATGGTGGGATGGTGCAGACTGTTTCAGACCAGGTACACATTTGGTGGCGCTCTGTTCTGTG  
 GGCTGGGTCGCTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGG  
 CCTGGCACCAGAAGAAACCACTACAAAGCCGTTTCTTATCATGCCCTCAGGCCACAGTGTG  
 CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAAACAAGAG  
 ATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTA  
 TGTG**TAA**TGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAA  
 AACAAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGC  
 CTCGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTCAATATTTCC  
 ACCATAAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTAT  
 TTCTTTTTTTAAATATAAATTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCAC  
 ATTTTGATGATTTAGACAGACTCCCCCTCTTCTCCTAGTCAATAAACCCATTGATGATCTA  
 TTTCCCAGCTTATCCCCAAGAAAACCTTTTGAAAGGAAAGAGTAGACCCAAAGATGTTATTTT  
 CTGCTGTTTGAAATTTTGTCCTCCCAACCCCAACTGGCTAGTAATAAACACTTACTGAAGAA  
 GAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTG  
 TGATCTTAAAGTTACCAAAACAAAGTCATTTTCAGTTTGAGGCAACCAACCTTTCTACTG  
 CTGTTGACATCTTCTATTACAGCAACACCATTTCTAGAGGTTCTGAGCTCTCCACTGGAG  
 TCCTCTTTCTGTGCGGGGTGAGAAATTGTCCCTAGATGAATGAGAAAAATTATTTTTTTTAAAT  
 TTAAGTCTTAAATATAGTTAAATAAATAATGTTTTAGTAAATGATACACTATCTCTGTGA  
 AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAATAATTGCTTTGACATTGTCT  
 ATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTCATGAAAAGCTCACACCTGTAATC  
 CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCGAGAAGTTCCGAGACTAGCCGTG  
 GGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAATCAGCCAGTCATGGTG  
 GCATACACCTGTAGTCCAGCATTCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCACGGG  
 AGGTTGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGA  
 TCCTGTCTAAAAAATAAAAAATAAATAATGGAACACAGCAAGTCTAGGAAGTAGGTTAA  
 ACTAATCTTTAA

**FIGURE 186**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734

><subunit 1 of 1, 261 aa, 1 stop

><MW: 27856, pI: 8.50, NX(S/T): 1

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTE  
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM  
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL  
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE  
DEVQSYPSKHDYV

**Signal peptide:**

amino acids 1-23

**Transmembrane domains:**

amino acids 81-100, 121-141, 173-194



**FIGURE 187**

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCGG  
 GAGTCCAGCTGGCTAAAACATCCCAGAGGATAATGCGCAACCCATGCCTTAGAAATCGCTG  
 GGCTGTTTCTTGGTGGTGTGGAAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGG  
 AGAGTGTGCGCCTTCATTGAAAAACAATCGTGGTTTTTGGAAACTTCTGGGAAGGACTGTG  
 GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGG  
 CTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTCCGTGATGTCCTTC  
 TTGGCTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGACAATGAGAA  
 GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC  
 TCATCCCTGTGAGCTGGGTGCCAATGCCATCATCAGAGATTCTATAACTCAATAGTGAAT  
 GTTGCCCAAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCCTGGTGCT  
 GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTGTGTTGCAACGAAAAGAGCAGTAGCTACA  
 GATACTCGATACCTTCCCATCGCACAAACCAAAAAGTTATCACACCGGAAAGAAGTCACCG  
 AGCGTCTACTCCAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTAACTTTACTATAAAAGC  
 CATGCAAAATGACAAAAATCTATATTACTTTTCTCAAAATGGACCCCAAGAAACTTTGATTTA  
 CTGTTCTTAACTGCCTAATCTTAATTACAGGAACGTGCATCAGCTATTTATGATTCTATAA  
 GCTATTTTCAGCAGAATGAGATATTAACCCAATGCTTTGATTGTTCTAGAAAGTATAGTAAT  
 TTGTTTTCTAAGGTGGTTCAAGCATCTACTCTTTTATCATTTACTTCAAAATGACATTGCT  
 AAAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG  
 TGTAAACATTTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAG  
 TCCATTACACTGAATAAATAGAAGTCAACTATTGCTTTTCAGGGAATCATGGATAGGGTTG  
 AAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCTCCATTTATAATGA  
 AGATTAATAATGAAGGCTTTAATCAGCATTGTAAAGGAAATGAATGGCTTTCTGATATGCTG  
 TTTTTCAGCCTAGGAGTTAGAAATCCTAATCTTTATCTCTCTCTCCAGAGGCTTTTTTT  
 TTCTTGTTGATTAAATTAACATTTTTTAAACGCGAGATATTTGTCAAGGGGCTTTGCATTCA  
 AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG  
 GTTTTAGGAAAGTGAAAAATTTTTGTTTTGTATTTGAAGAAGATGATGCATTTTGACAA  
 GAAATCATATATGATGGATATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC  
 AATAATAAATAAAGAGCAGAAAAATATGTCTTGGTTTTTCATTGTGCTTACCAAAAAACAACA  
 ACAAAAAAGTTGTCCTTTGAGAAGTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATTG  
 TCATTTTTGTCTGTGAAAAATAAATTTCTTCTGTACCATTTCTGTTAGTTTTACTAAA  
 ATCTGTAAATACTGTATTTTTCTGTTTATTCAAATTTGATGAAACTGACAATCCAATTTGA  
 AAGTTTGTGTCGAGCTGTCTAGCTTAAATGAATGTGTTCTATTGCTTTATACATTTATA  
 TTAATAAATTGTACATTTTTCTAATT

**FIGURE 188**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735
><subunit 1 of 1, 225 aa, 1 stop
><MW: 24845, pI: 9.07, NX(S/T): 0
MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM
QCKIYDSLALLSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI
IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV
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**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

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**FIGURE 189**

TCGCC**ATG**GCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCCTGACACTGCTGGGCTGGGTG  
AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT  
CGTGGTGGCCAGGTGGTGTGGGAGGGCCTGTGGATGTCTCGTGGTGCAGAGCACCGGCC  
AGATGCAGTGAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT  
GCCCTCTGTGTATCGCCCTCCTTGTGGCCCTGTTGCGCTTGTGGTCTACCTTGTGGGGC  
CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGCTCACCTCTGGGA  
TTGTCTTTGTATCTCAGGGGTCTGACGCTAATCCCCGTGTGCTGGACGGCGCATGCCATC  
ATCCGGGACTTCTATAACCCCCCTGGTGGCTGAGGCCAAAAGCGGGAGCTGGGGGCTCCCT  
CTACTTGGGCTGGGCGGCCTCAGGCCTTTTGTGCTGGTGGGGGTGCTGTGTGCACTT  
GCCCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCCGCTACTCAACATCTGCCCT  
GCCATCTCTCGGGGGCCCTCTGAGTACCCTACCAAGAATTACGCT**TGA**CGTGGAGGGGAATG  
GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGTT  
CGTACCTTTTGTCTCTGCTCCTGTATTTTCTTTTGGACTGAGGATATTTAAATTCATTT  
GAAACTGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCCCTTGG  
ATGATGGAGCCAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCCATCTTAGAAGC  
CAGTCAAGCTATGGAACTAATGCGGAGGCTGCTTGCTGTGCTGGCTTGCAACAAGACAGAC  
TGTCCCCAAGAGTTCTGCTGCTGCTGGGGGCTGGGCTTCCCTAGATGTCACTGGACAGCTG  
CCCCCATCTACTCAGGTCTCTGGAGCTCCTCTCTTACCCCTGGAAAAACAAATCATCTG  
TTAACAAAGGACTGCCACCTCCGGAACCTCTGACCTCTGTTTCCCTCCGCTGATAAGACG  
TCCACCCCCCAGGGCCAGGTCCAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC  
CTTCTGCCCTGCCCCCTCGTCTACCCCTTTACACTCACATTTTATCAAATAAAGCATG  
TTTTGTTAGTGCA



**FIGURE 190**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736
><subunit 1 of 1, 220 aa, 1 stop
><MW: 23292, pI: 8.43, NX(S/T): 0
MASAGMQILGVVLTLLGWVNLVSCALPMWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQM
QCKVYDSLALPQDLQAARALCVIALLVALLFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV
FVISGVLTLIPVCWTAHAIIRDFYNPLVAEAQKRELGAISLYLGWAASGLLLGGGLLCCTCP
SGGSQGPPSHYMARYSTSAPAIRGPSEYPTKNYV
```

**Transmembrane domains:**

amino acids 8-30 (type II), 82-102, 121-140, 166-186

**FIGURE 191**

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAGGCTTCCACGTTCTACATCTTG  
 AGCATCTTCTACCACTCCGAATTGAACCACTCTTCAAAGTAAAGGCAATGGCATTATCCC  
 TTGCAAATTGCTGGGCTGGTTCTTGGGTTCTTGGCATGGTGGGACTCTTGCCACAACCCCT  
 TCTGCCCTCAGTGGTGGAGTATCAGCTTTTGTGGCAGCAACATTATTGTCTTTGAGAGGCTC  
 TGGGAAGGGCTCTG**CATGA**AATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA  
 TAGTCCCTTGTGGCTCTCCCGCTGCCCTGGAAACAGCCGGGCCCTCATGTGTGTGGCTG  
 TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA  
 GGCTCTAACGAGAGGGCCAAAGCATACCTTCTGGGAACCTCAGGAGTCCTCTTCATCCTGAC  
 GGGTATCTTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTTCTACA  
 ACCCAGCCATCCACATAGGTGAGAAACGAGAGCTGGGAGCAGCACTTTTCTTGGCTGGGCA  
 AGCGCTGCTGTCCCTCTTCATTGGAGGGGGTCTGCTTTGTGGATTTTGTCTGCTGCAACAGAAA  
 GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA  
 ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGCTC**TAA**TGCCTCCTTTTGGCTCCAAGT  
 ATGGACTATGGTCAATGTTTTTATAAAGTCCTGCTAGAAACTGTAAGTATGTGAGGCAGGA  
 GAACTTGCTTTTATGTCTAGATTACATTGATACGAAAGTTCAATTTGTTACTGGTGGTAGG  
 AATGAAAATGACTTACTTGGACATTCTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG  
 GACCCAATCGCTGCTCCAATTTTCATATTCTAAATTCAAGTATACCCATAATCATTAGCAAG  
 TGTACAATGATGGACTACTTATTACTTTTTGACCATCATGTATTATCTGATAAGAATCTAAA  
 GTTGAAATTGATATTCTATAACAATAAACATATACCTATTCTA

**FIGURE 192**

```
>>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737
>>subunit 1 of 1, 173 aa, 1 stop
>>MW: 18938, pI: 9.99, NX(S/T): 1
MNCIRQARVRVLQCKFYSSLLALPPALETARALMCVAVALSLIALLLIGICGMKQVQCTGSNER
AKAYLLGTSGVLFILTGIFVLVPSWTANIIRDFYNPAIHIGQKRELGAALFLGWASAVAL
FIGGGLLCGFCCCNRRKKQGYRYPVPGYRVPHTDKRRNTTMLSKTSTSYV
```

Important features of the protein:

Transmembrane domains:

amino acids 31-51, 71-90, 112-133

N-glycosylation site.

amino acids 161-164

**FIGURE 193**

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGC**ATGA**AAGATCACTGGGGGT  
 CTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC  
 AAAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCA  
 CATACCTACCAGTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACTTGTGTACC  
 GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGCT**TAA**ATTCTCCA  
 TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTG  
 AGTTTCITTCAGTTTACTGATGTTCTGGGTGGGGACAGAGCCAGATTAGAGTAATCTTG  
 ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAACCCTATGCCTCACTGACAGACCAGCAT  
 TTTTTTTTAAACAGTCAATAAAAAAATAATCTCCAGA

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**FIGURE 194**

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><subunit 1 of 1, 85 aa, 1 stop

><MW: 9232, pI: 7.94, NX(S/T): 0

MKITGGLLLCTVVYFCSSEEAASLSPKKVDCSIYKYPVVAIPCPITYLPVCGSDYITYGN  
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**FIGURE 195**

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCC  
 CGCCGCC**CATG**GCTGCCTCCCCGCGCGGCTGCTGTCTGGCCCTGACCGGGCTGGCGCTGC  
 TCCTGCTCCTGTGCTGGGGCCAGGTGGCATAAGTGAAATAAACTCAAGCTGATGCTTCAA  
 AACGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGA  
 ATTCTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCGAGGTGC  
 AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC  
 ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA  
 CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCTACGGCTTTAGGCATGGAGCCAGCG  
 TCAACTACGATGACTACT**TAA**CCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATTCT  
 TCTTCATGTATCTCCTAATGCCTTACACTACTTGTTTTCTGATTGTCTATTTTCAGCAGAT  
 CTTTTCTACCTACTTTGTGTGATCAAAAAAGAAGAGTTAAACAACACATGTAAATGCCTTT  
 TGATATTTCATGGGAATGCCTCTCATTAAAAATAGAAATAAAGCATTGTTAAAAAGA

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**FIGURE 196**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLLCWGPGGISGNKCLKMLQKREAPVPTKTKVAVDENKAKEFL  
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNRNGHEYYGDIYQRHYD  
EDSAIGPRSPYGFRRHGASVNYDDY

**Signal peptide:**

amino acids 1-30

**FIGURE 197**

CGGCTCGAGCCCGCCCGGAAGTGCCCGAGGGGCCGCGATGGAGCTGGGGGAGCCGGGCGCTC  
 GGTAGCGCGCGGGCAAGGCAGGCGCC**ATG**ACCCTGATTGAAGGGGTGGGTGATGAGGTGAC  
 CGTCCTTTTCTCGGTGCTTGCCGCTTCTGGTGCTGGCCCTTGCCGGGTCTCAACGCACA  
 CCGCTGAGGGCGGGGACCCACTGCCCCAGCCGTAGGGGACCCCAACGCCATCCCAGCCCAGC  
 GCAGCCATGGCAGCTACCGACAGCATGAGAGGGGAGGCCCCAGGGGCAGAGACCCCGAGCCT  
 GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCAGCACGGGTTTACAGCAACACCGCCAG  
 CCCC GGACTCCCCGAGGAGCCCTCGTGCTACGGCTGAAATTCCTCAATGATTCAGAGCAG  
 GTGGCCAGGGCCTGGCCCCACGACACCATTTGGCTCCTTGAAAAGGACCCAGTTTCCCGGCCG  
 GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCCTGG  
 GCAGCCTTACCTCCCTCCCAACTGCGTTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC  
 CCAAATCCCCCTGCCCGCCGGGGTCCGAGCCCGGCCCTCCGGGCTGGAATTCGGCAGCCT  
 GCTGCTGCCCTGCTGCTCCTGCTGTGCTGCTGCTGCTGGTACTGCCAGATCCAGTACCGGC  
 CCTTCTTTCCCTGACCGCCACTCTGGGCTGGCCGGCTTACCCGTCTCCTCAGTCTCCTG  
 GCCTTTGGCATGTACCGCCCG**TAG**TGCCTCCGCGGGCGCTTGGCAGCGTCGCCGGCCCTCC  
 GGACCTTGCTCCCCGCGCCGCGGGAGCTGCTGCCTGCCAGGCCCGCCTCTCCGGCCTG  
 CCTCTTCCCGCTGCCCTGGAGCCCCAGCCCTGCGCCGACAGGACTCCCGGGACTGGCGGAGG  
 CCCCCCCTGCGACCGCCGGGGTTCGGGGCCACCTCCCGGGGCTGCTGAACCTCAGCCGCA  
 CTGGGAGTGGGCTCCTCGGGTTCGGGCATCTGCTGTCGCTGCTCGGCCCGGGCAGAGCCG  
 GGCGCCCCGGGGGCCGCTTCTAGTGTCTGCCGGAGACCCAGCCGCTCCAAATCCCTGAC  
 AGCTCCTTGGGCTGAGTTGGGGACGCCAGGTCGGTGGGAGGCTGGTGAAGGGAGCGGGGAG  
 GGGCAGAGGAGTTCCCCGGAACCCGTGCAGATTAAAGTAACTGTGAAGTTTAAAAAAAAA  
 AAAAAAA



**FIGURE 198**

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM  
 RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVLRCLKFLNDSEQVARAWPHDT  
 IGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPCCPPGS  
 EPGFSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLLLSLLAFAMYRP

**Signal peptide:**

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**Transmembrane domain:**

amino acids 195-217

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**FIGURE 199**

GAGATTGGAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG  
 ATCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCTAAGAACCATCAGCCC  
 TCAGCTGCACCTCCTCCCCTCCAAGGATGACAAAGGCGCTACTCATCTATTTGGTCAGCAGC  
 TTTCTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCT  
 GGAGGACTTGGATGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTTGTGG  
 AAAGCAAGTTCAACATATCAAAGATAAATGAAAATGCGGATGGAAGCTTTGACTATGGCCTC  
 TTCCAGATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTTGCCA  
 CGTAGACTGTCAAGATCTGCTGAATCCCAACCTTCTTGAGGATCCACTGCGCAAAAAGGA  
 TTGTGTCCGGAGCACGGGGGATGAACAACCTGGGTAGAATGGAGGTTGCACGTTCAGGCCGG  
 CCACTCTCCTACTGGCTGACAGGATGCCGCCTGAGATGAACAGGGTGCGGGTGACCGTGG  
 AGTCATTCCAAGACTCCTGTCCTCACTCAGGGATTCTTCATTCTTCTTCTACTGCCTCCA  
 CTTTCATGTTATTTTCTTCCCTTCCCATTACAACTAAAAGTACCAGAGCCCCAGGAATAAA  
 TGGTTTTCTTGGCTTCTCCTTACTCCCATCTGGACCCAGTCCCCTGGTTCTGTCTGTTAT  
 TTGTAACTGAGGACCACAATAAAGAAATCTTTATATTTATCG

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**FIGURE 200**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI  
NENADGSFDYGLFQINSHYWCNDYKSYSENLCHVDCQDLLNPNNLAGIHCAKRIVSGARGMN  
NWVEWRLHCSGRPLSYWLTGCRLR

**Signal peptide:**

amino acids 1-18

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99. ch  
100. ch

**FIGURE 201**

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTACGCCCTGCTTGACTGAGAACCCA  
 CCAGCTCATCCACAGACCTCATAGCAACCTATTATTACAAAGGGGGAAAGAAACACCTGAG  
 CAGAATGGAATCATATTATTTTTTCCCAAGGAGAAAACCGGGTAAAGGGAGGGAAGCAATTC  
 AATTGGAAGTCCCTGTGAATGGGCTTTCAGAAGGCAATTAAGAAAATCCACTCAGAGAGGAC  
 TTGGGGTGAAACTTTGGGTCCTGTGGTTTTCTGATTGTAAGTGAAGCAGGTCCTTGACACACGC  
 TGTGGGCAATGTGAGGACCAGGTTAAGTGACTGGCAGAAAACTTCCAGGTGGAACAAGCA  
 ACCCATGTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGAC  
 CTGTTGCATTGGCAAGTTCTAGCAACATGCTCCTAAGGAAGCGATACAGGCACAGACCATG  
 CAGACTCCAGTTCCCTGCTGCTCCTGATGCTGGGATGCGTCTCTGATGATGGTGGCGATGT  
 TGCACCTCCCCACCACACCTTGACACAGACTGTACAGCCCAAGCCAGCAAGCAGGCCCT  
 GAAGCCAGGTACCGCTGGAATTTGGGGAATCCCAGGATTTGGGTACTGGAAGCTGAGGATGA  
 GGGTGAAGAGTACAGCCCTCTGGAGGGCTTGCACCTTTATCTCACTGCGGGAGGATCAGC  
 TGCTGGTGGCCGTGGCCTTACCCAGGCCAGAAGGAACAGAGCCAGGGCAGGAGAGGTGGG  
 AGCTACCGCCTCATCAAGCAGCAAGGAGGCAAGGATAAGGAAGCCCCAAAGAGGGAAGTGGG  
 GGCTGATGAGGACGGGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTACGCTGGACCCAC  
 GTGGCCTCCAGGAGGCACTCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCCGAGGTGCGG  
 CACCCACTGTGTCTGCAGCAGCACCTCAGGACAGCCTGCCACAGCCAGCGTATCCTCTGT  
 TTTCATGATGAGGCTGTGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGC  
 CCAGGGCCTTCTCTGAAGGAGATCATCTCTGTCGACGACCTCAGCCAGCAAGGACAACCTCAAG  
 TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGTGAAGTTACTCAGGAGCAACAAGAG  
 GCTGGGTGCCATCAGGGCCCCGATGCTGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCT  
 TCATGGATGCCCACTGCGAGTGCCACCCAGGCTGGCTGGAGCCCTCTCAGCAGAAATAGCT  
 GGTGACAGGAGCCGAGTGGTATCTCCGGTGATAGATGTGATTGACTGGAAGACTTTCAGTA  
 TTACCCCTCAAAGGACCTGCAGCGTGGGGTGTGGACTGGAAGCTGGATTTCCTACTGGGAAC  
 CTTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCATAAGCCCCATCAGAGGCCCTGTG  
 GTGCCCGGAGAGGTGGTGCCATGGACAGACATTACTTCCAAAACACTGGAGCGTATGACTC  
 TCTTATGTCTGCTGCGAGGTGGTGAACACCTCGAAGTGTCTTTCAAGGCCCTGGCTCTGTGGTG  
 GCTCTGTTGAAATCCTTCCCTGCTCTCGGGTAGGACACATCTACCAAAATCAGGATTTCCCAT  
 TCCCCCTCGACAGGAGGCCACCTTGAGGAACAGGGTTTCGATTTGCTGAGACCTGGCTGGG  
 GTCATTCAAAGAAACCTTCTACAAGCATAGCCAGAGGCCCTTCTCTTGAGCAAGGCTGAGA  
 AGCCAGACTGCATGGAACGCTTGACGTGCAAAGGAGACTGGGTGTGCGACATTCCACTGG  
 TTTCTGGCTAATGTCTACCTGAGCTGTACCCATCTGAACCCAGGCCCCAGTTTCTCTGGAAG  
 GCTCCACAACACTGGACTTGGGCTCTGTGCAGACTGCCAGGCAGAGGGGACATCTCGGGCT  
 GTCCATGTTGTTGGCTCCTTGCACTGACAGCCGGCAGCAACAGTACCTGCGACACACAGC  
 AGGAAGGAGATTCACTTTGGCAGGCCACAGCACTGTGCTTTGCTCAGGCAAGGACAGGT  
 GATTCTTCAGAACTGCACGGAGGAAGGCCGTGGCCATCCACAGCAGCACTGGGACTTCCAGG  
 AGAATGGGATGATTGTCCACATTTCTTCTGGGAAATGCATGGAAGCTGTGGTGCAAGAAAAA  
 AATAAAGATTGTACCTGCCGTCCGTGTGATGGAAGAAAGCCCCCAGCAGTGGCGATTGGAAC  
 GATAAATGCTGTGGATGAACGATGAATGTCAATGTGAGAAGGAAAGAGATTTTGGCCATC  
 AAAATCAGCTCCAAAGTGAACGTAAGAGCTTATATATTTTATGAAGCTGATCCTTTTGTGT  
 GTGTGCTCCTTGTGTTAGGAGAGAAAAAGCTCTATGAAGAATATAGGAAGTTTCTCCTTT  
 TCACACCTTATTTCATTGACTGCTGGCTGCTTA

**FIGURE 202**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760

><subunit 1 of 1, 639 aa, 1 stop

><MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQTVTAQASKHSPEARYRLDFG  
ESQDWVLEAEDEGEYSPLGLEPFFISLREDQLLVAVALPQARRNQSQGRGGSYRLIKQPR  
RQDKEAPKRDWGADEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP  
QDSLPTASVILCFHDEAWSTLLRRTVHSILDTPVPRFLKEIILVDDLQSQGQLKSALSEYVAR  
LEGVKLLRSNKRLGAIRARMLGATRATGDLVLFMDAHCECHPGWLEPLLSRIAGDRSRVVS  
VIDVIDWKTQYYPSKDLQRGVLDWKLDHFHWEPLPEHVRKALQSPISPIRSEVVPGEVVAMD  
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHYQNDSDHSPLDQEATL  
RNRVRIAETWLGSFKETFYKHSPEAFSLSKAEKPDCEMERLQLQRRLCRTFHWFLANVPEL  
YPSEPRPSFSGKLHNTGLGLCADCQAEGDILGCPMVLAPCSDSRQQYLOHTSRKEIHFGSP  
QHLCFAVRQEQQVILQNCTEEGLAIHQHWDQENGMIHVHILSGKCMEEAVVQENNKDLYLRPC  
DGKARQQWRFDQINAVDER

**Signal peptide:**

amino acids 1-28

**FIGURE 203**

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACACAGCTGAGGAAGACCTCAGACATGGA  
 GTCCAGGATGTGGGCTGCGCTGCTGCTGTCCCACCTCCTCCCTCTCTGGCCACTGCTGTTGC  
 TGCCCCCTCCACCGCTGCTCAGGGCTCTTTCATCCTCCCTCGAACCCACCAGCCCCAGCC  
 CGCCCCCGTGTGCCAGGGGAGGCCCTCGGCCCCACGTCATGTGTGGCGTGTGGGAGCGGAGC  
 ACCCTCCACCAAGCCGATCTCCTCGGGTCCCAAGATCAGCTCGGCAAGTCTGCTGCGCCATG  
 CACCCCCAGCCACCCCATCAGGCTTTGAGGAGGGGCGGCCCTCATCCCAATACCCCTGGGCT  
 ATCGTGTGGGGTCCACCGTGTCTCGAGAGGATGGAGGGGACCCCAACTCTGCCAATCCCGG  
 ATTTCTGGACTATGGTTTTGACGCCCTCATGGGCTCGCAACCCACACCCCAACTCAGACT  
 CCATGCGAGGTGATGGAGATGGGCTTATCCTTGGAGAGGCACCTGCCACCCCTCGCGCCATT  
 CTGTTTCGGGGGCGGTGGGGAAGGTGTGGACCCCAAGCTCTATGTCACAATTACCATCTCCAT  
 CATCATTTGTTCTCGTGGCCACTGGCATCATTTCAAGTTCTGCTGGGACCGCAGCCAGAAGC  
 GACGCAGACCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGAGCCAGCCAGCCACTGACA  
 GACCTGTCCCGGCTGGAGTCACTGTGCTGGGGGCTTCGGGGGACTCACCTACCCCAACCC  
 TGACCATGAGGAGCCCCGAGGGGACCCCGCCTGGGATGCCCCACCCCAAGGGGGCTCCAG  
 CCTTCCAGTTGAACCGGTGAGGGGAGGGGCAATGGGATGGGAGGGCAAAGAGGGAAGGCAAC  
 TTAGGCTCTTCAGAGCTGGGGTGGGGTGGCCCTCTGGATGGGTAGTGAGGAGGCAGGCGTGGC  
 CTCCACAGCCCTTGGCCCTCCCAAGGGGGCTGGACCAAGCTCCTCTCTGGGAGGCACCTTCT  
 CTTCTCCAGTCTCTCAGGATCTGTGTCTTATCTCTGCTGCCCATAACTCCAACCTCTGCC  
 TCTTTGGTTTTTTCTCATGCCACCTTGCTTAAGACAACCTCTGCCCTCTTAACCTTGATTCCC  
 CCTCTTTGTCTTGAACCTTCCCCTTCTATTCTGGCCTACCCCTTGGTTCTGACTGTGCCCTT  
 TCCCTCTTCTCTCAGGATTCCTTGGTGAATCTGTGATGCCCAATGTTGGGGTGCAGCC  
 AAGCAGGAGGCCAAGGGGCGGCAAGCCCACTCCCACTGAGGGTGGGGCAGCTGTGGGGA  
 GCTGGGGCCACAGGGGCTCCTGGCTCCTGCCCTTGACACACCACCCGGAACACTCCCCAGCC  
 CCACGGGCAATCCTATCTGCTCGCCCTCCTGCAGGTGGGGGCTCACATATCTGTGACTTCG  
 GGTCCCTGTCCCCACCTTGTGCACCTCACATGAAAGCCTTGACACTCACTCCACCTTCCAC  
 AGGCCATTTGCACACGCTCCTGCACCTCTCCCGTCCATACCGCTCCGCTCAGCTGACTCT  
 CATGTTCTCTCGTCTCACATTTGCACTCTCTCTTCCCACATTTCTGTCTCAGCTCACTCAG  
 TGGTCAGCGTTTCTGACACACTTTACCTCTCATGTGCGTTTCCCGGCCCTGATGTTGTGGTGG  
 TGTGCGGCGTGTCACTCTCTCCTCATGAACACCCACCCACCTCGTTTCCGAGGCCCTGCG  
 GTGCTGCTCCAGAGGTGGGTGGGAGGTGAGCTGGGGGCTCCTTGGGCCCTCATCGGTCAITG  
 TCTCTGTCCTTCCACACCATTTGTTTCTCTGTCTCCCCATCCTACTCCAAGGATGCCGGCA  
 TCACCTGAGGGCTCCCCCTTGGGAATGGGGTAGTGAGGGCCAGACTTCACCCCCAGCCCA  
 CTGCTAAAATCTGTTTTCTGACAGATGGGTTTTGGGGAGTCGCCCTGCTGCACATACATGAGAA  
 AGGGACTCCCATTTGGCCTTCCCTTCTCCTACAGTCCCTTTTGTCTTGTCTGCTCCTGGCTG  
 TCTGTGTGTGCCATTCTCTGGACTTCAGAGCCCTGAGCCCTTCCCTTCCCTTCCAGGCT  
 CCCTTGGGGCTCCCTAACTCCACCTAGGCTGCCAGGACCGGAGTCAGCTGTTTCAAGGCC  
 ATCGGAGGCTCTGCCTCCAAGTCTACCCCTCCCTTCCCGGACTCCCTCCTGTCCCCCTCCTTT  
 CCTCCCTCCTTCCCTTCCACTCCTTCCCTTCTTGTCTTCCCTTCCCTTCCCTTCCCTGAGGT  
 CTTCCTCTCTTCTCACTGTTTTTCCACCTTCTCTTCCCTTCCCTTCCCTTCCCTGAGGT  
 GTGATATATATTTTTGTATTATCTCTTCTTCTTCTTGTGATCATCTTGAATTACTGTG  
 GGATGTAAGTTTCAAATTTTCAAATAAGCCTTTGCAAGATA

**FIGURE 204**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKQLRQREVVDLYNGMCLQGPGAV  
 PGRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA  
 ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEATIIYLDQGSPEMN  
 STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNVSRIIEELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

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**FIGURE 205**

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGGATGG  
CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCCCTGCGGTG  
CTCACAGACGATGTTCCACAGGAGCCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC  
GTCGGGAGAAAGCCCCGTGGAGAGCACCAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCC  
CAGCCCCCACCGTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGC  
GGCGGGTCGCTGGGGCCCGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG  
CGTGGTGCTGGCGCTCGTGGTCGTCGCGCTGAGAAAGTTTTCTGCCTCCTGAAGCGAATAAA  
GGGGCCGCGCCCGCCGCGCGCGACTCGGCAAAAAAAAAAAAAA



**FIGURE 206**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEFAELPSGEGPVESTSPGREPVDTG
PPAPT VAPGPE DSTAQERLDQGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS
```

**Important features of the protein:****Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 91-110

**Glycosaminoglycan attachment site.**

amino acids 44-47

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 116-119

**N-myristoylation site.**

amino acids 91-96

**FIGURE 207**

GGCCGTTGGTTGGTGC GCGCGCTGAAGGGTGTGGCGCAGCAGCGTCGTTGGTTGGCCGGCGG  
 CGGGCCGGGACGGGC**ATG**GCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCCA  
 CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA  
 ACTTCAAGTCCTGGTGGGTGGGCGACATCCCCGTGTGAGGGGCGCTGCTACCGACTGGAGC  
 GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGA  
 CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC  
 CCGGGTATTTCCTCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC  
 GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGG  
 ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGCGGGGACCTCCCC**TAA**GTAGCCC  
 CCAGAGGCGCTGGGAGTGTTGCCACCGCCCTCCCTTGAAGTTTGCTCCATCTCACGCTGGGG  
 GTCAACCTGGGGACCCCTTCCCTCCGGGCCATGGACACACATACATGAAAACAGGCCGCAT  
 CGACTGTGACACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACTGCACAG  
 ACTCGCAGCTCGCCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGT  
 GCCAGGGCCCTACTGTCCCTGGGGTCCCAGGCTCTCCTTGAGGGGGGCTCCCGCCTTCCAC  
 CTGGCTGTGATCGGGTAGGGCGGGCCGTGGGTTGAGGGGCGCACCACTTCCAAGCCTGTGT  
 CCCACAGGTCCTCGGCGCAGTGGAAAGTCAGCTGTCCAGGGCCTCCTGAACTACATAAATAAC  
 TGGCACAAGTAAGTCCCTCCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTG  
 GGTGAGTATGTGTGGGGCACAGGCTGGCTCCCTCAGCTCCCACGTCTAGAGGGGCTCCCGA  
 GGAGGTGGAACCTCAACCCAGCTCTGCGCAGGAGGCGGCTGCAGTCCTTTTCTCCCTCAAAG  
 GTCTCCGACCCTCAGCTGGAGGCGGGCATCTTCTCAAAGGGTCCCATAGGGTCTGGTTCC  
 ACCCATCCAGGCTGTGGTCAAGCCTGGGAGGGTCCCTACGATGGTTAGGGGTGCCCC  
 ATGGAGGGGCTGACTGCCCCACATTGCCTTTCAGACAGGACACGAGCATGAGGTAAAGCCGC  
 CCTGACCTGGACTTCAGGGGGAGGGGGTAAAGGGAGAGAGAGGGGGGGCTAGGGGGTCTCT  
 AGATCAGTGGGGGCATGTCAGGTGGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCAC  
 CTCTGCAACCACACCCATGTGGTGGTTTCATGAACAGACCAGCTCCTCTGCCTTCTCCTGG  
 CCTGGGACACACAGAGCCACCCCGGCCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGA  
 AGGGGTGCTCGTAAGCCAACACCAGCGTGCCGCGGCCTGCACACCCCTTCGGACATCCAGGC  
 ACGAGGGTGTCTGGATGTGGCCACATAGGACCACAGTCCAGCTGGGAGGAGAGGCCT  
 GGGGCCCCAGGGAGGAGGACGGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC  
 CCGCAGCCTGGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCACACTTGGCCAACTGACCT  
 TGGAAAGATGCTGTGAGTGTCTAAGCAGCACTGACAGCAGCTGGGCCTGCCCAGGGCAAC  
 GTGGGGGCGGAGACTCAGCTGGACAGCCCTGCCTGTCACTCTGGAGCTGGGCTGTGCTGC  
 CTCAGGACCCCTCTCCGACCCCGGACAGAGCTGAGCTGGCCAGGGCCAGGAGGGCGGGAGG  
 GAGGGAATGGGGGTGGGCTGTGCGCAGCATCAGCGCTGGGCAGGTCCGACAGCTGCGGGA  
 TGTGATTAAAGTCCCTGATGTTTCTC

**FIGURE 208**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK  
ELHLAIPAKITREKLDQVATAVYQMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIER  
HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDLF

**Signal peptide:**

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**FIGURE 209**

AGCAGGAGCAGGAGAGGGACA**ATGGA**AGCTGCCCCGTCCAGGTTTCATGTTCTTCTTATTCT  
 CCTCACGTTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCTCTG  
 GTGCTGCCCAGGAACCCACGTGGCTCACAGATGTCCAGCTGCCATGGAATTCATTGTGCTGCC  
 ACTGAGGTGGCTGTTCATAGGCTTCTTCCAGGATTAGAAAATACCAGCAGTGCCCATATCCCA  
 TAGCATGGTGCAAAAATTCCAGGCGTGTTCATTGGGATCAGCACTGATTCTGAGGTTCTGA  
 CACACTACAACATCACTGGGAACACCATCTGCCTCTTTCGCCTGGTAGACAATGAACAACTG  
 AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGAT  
 CAACAGCCTCCACATGGTGACAGAGTACAACCCGTGACTGTGATTGGGTTATTCAACAGCG  
 TAATTCAGATTTCATCTCCTCCTGATAATGAACAAGGCCCTCCCAGAGTATGAAGAGAACATG  
 CACAGATACCAGAAGGCAGCCAAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAG  
 TGGTATGAAAGAAAAATGGGAAGGTGATATCATTTTTTCAAACATAAGGAGTCTCAAACGCCAG  
 CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATACACTGCCACAGCAGAAGTTTCC  
 GTAGAGCATGTGCAAAATTTTGTGATGGATTCTAAGTGGAAAATTGTTGAAAGAAAAATCG  
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAACCT**TGA**CTTCTCCTTGGAACATACATATGGCC  
 AAGTATCTACTTTATGCAAAGTAAAAAGGCACAACTCAAATCTCAGAGACACTAAACAACAG  
 GATCACTAGGCCGTGCCAACACACACACACAGAGCTTCATTTCTGTCTTAAAAATCTCGTTTTCTC  
 ACACACGCGCACACACACACACACAGAGCTTCATTTCTGTCTTAAAAATCTCGTTTTCTC  
 TTCTTCTCTTTTAAATTTTCATATCTCTACTCCCTATCCAATTTCTTCTTATCGTGCATT  
 CATACTCTGTAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG  
 CCTCTATGAAAGAGAGGCATTCTTAGAGAAAGATTGTTCCAATTTGTCAATTAATATCAAGT  
 TTGTATACTGCACATGACTTACACACAACATAGTTCTGCTCTTTTAAGGTTACCTAAGGGT  
 TGAAACTCTACCTTCTTTTCATAAGCAGCATGTCCGTCTCTGACTCAGGATCAAAAACCAAGG  
 ATGGTTTTAAACACCTTTGTGAAATTGTCTTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC  
 CCTGAACTCAGCAGAAATAGACCATGTGAAAACCTCCATGCTTGGTTAGCATCTCCAACCTCC  
 TATGTAAATCAACAACCTGCATAATAAATAAAGGCAATCATGTTATA

**FIGURE 210**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30480, pI: 4.60, NX(S/T): 1

MEAAPSRFMFLFLLTCELAEEVAAEVEKSSDGPAAQEPTWLTDVPAAMEFIAATEVAVIG  
 FFQDLEIPAVFILHSMVQKFPGVSGISTDSEVLTHYNITGNTICLFRLDVNEQLNLEDEDI  
 ESIDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLILLIMNKASPEYEENMHRYQKAA  
 KLFQGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDDEWDTLPTAEVSVVEHVQNF  
 CDGFLSGKLLKENRESEGKTPKVEL

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 143-162

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**FIGURE 211**

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGGCGTGGAGGTGCCACCCGGCGCGGGTG  
 GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG  
 GACGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACG**ATG**GCAGCGTCCGCCGAGCCGGG  
 GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTGGTGTGCGCGCGGCGCTTGG  
 GCTCTTGACAGCTGGAGTATCAGCCTTGGAAGTATATACGCCAAAAGAAATCTTCGTGGCAA  
 ATGGTACACAAGGAAGCTGACCTGCAAGTTCAGTCTACTAGTACGACTGGCGGGTTGACC  
 TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTCGTTTTTCCACTACTC  
 CCAAGGGCAAGTGTACCTTGGGAATTATCCACCATTAAAGACAGAATCAGCTGGGCTGGAG  
 ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAAATATGCAGTTTATACACAATGGCACC  
 TATATCTGTGATGTCAAAAACCCCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTA  
 TGTCTGATAGAAAAAGAAATTTGCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG  
 CTGTGGTCTCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCTCTATAGAAGGAAA  
 AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTGTCAACAGTTAAGCAGGC  
 TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACC  
 AGGGCCCAAGTCATATATGCACAGTTAGACCCTCCGGCGGACATCAGTGACAAGATTAAC  
 AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAAT**TAA**GAGAATACCTAGAACATATC  
 CTCAGCAAGAAACAAAACCAAAGTGGACTCTCGTGACAGAAAATGTAGCCCATTAACCATGT  
 AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAAGTGTGT  
 ACAAGGATATGTATAAATATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTGCATGA  
 TGAAAAGATGGTATGATTCTACATATGTACCATTTGTCTGTGTTTTGTACTTTCTTTTC  
 AGGTCATTTACAATTGGGAGATTTAGAAAACATTCTTTTACCATCATTTAGAAATGGTTTG  
 CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAG  
 GGCTTAAGACTGATTAGTCTTAGCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA  
 GCATACCCAGGGTGGCCTTTAGCACAGTATCAGTACCATTATTTGTCTGCCGCTTTTAAAA  
 AATACCCATTGGCTATGCCACTTGAAAACAATTTGAGAAGTTTTTTTGAAGTTTTTCTCACT  
 AAAATATGGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCCTTG  
 AAATGTGTATATCAATTTCTGGATTCTAATAGCAAGATTAGCAAAGGATAATGCCGAAG  
 GTCATTCTATTCTGGACAGTTGGATCAATACTGATTAAGTAGAAAAATCCAAGCTTTGCTT  
 GAGAAGTTTTGTAACTGGAGAGTAAAAAGTATCGGTTTTA

**FIGURE 212**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510
```

><subunit 1 of 1, 269 aa, 1 stop

><MW: 29082, pI: 9.02, NX(S/T): 3

MAASAGAGAVIAAPDSDRRRLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS  
TSTTGGLTTSVSWSFQPEGADTTVSFFHYSGQGVYLGNYPPFKDRISWAGDLDDKKDASININEN  
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMI  
LAVLYRRKNKSRDYTCGSTESLSPVKQAPRKSPSDTEGLVKSLSFGSHQGPVIYAQLDHS  
GHSHDKINKSESVVYADIRSL

Signal peptide:

amino acids 1-37

**Transmembrane domain:**

amino acids 161-183

**FIGURE 213**

GCCGGCTGTGCAGAGACGCC**ATGT**TACCGGCTCCTGTGCAGCAGTGACTGCCCGGGCTGCCGCC  
 CCCGGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGCTGCCGCC  
 TCTCGGCCACGGCTGGGTGCGGGGCCCTCGGGCTGGGGCTGGGGCTGCGCGCTCGGGGTGAAGC  
 TGGCAGGTGGGCTGAGGGGCGCGGGCCCCGCGCAGTCCCCCGGGCCCCGACCCCTGAGGCG  
 TCGCCTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCCGGC  
 GCCGCCCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA  
 TCAAGGATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAGAAGTC  
 TGGTCAGAAGGTTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAAACCAGAGACAGT  
 TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTGCCAAATTGTGGGAAG  
 CAGGGAAACTGGATCTTGATATTCCAGTACAACATTATGTTCCCGAATTCCCGAAAAAGAA  
 TATGAAGGTGAAAAGGTTTCTGTCAACAAGATTACTGATTTCCCATTTAAGTGGAATTCG  
 TCATTATGAAAAGGACATAAAAAAGGTGAAAGAAAGAGAAAGCTTATAAGCCCTGAAGATGA  
 TGAAGAGAAATGTTGCATTTGAGCAAGAAAAAGAAGGCAAAAGTAATGAAAAGAATGATTTT  
 ACTAAATTTAAACAGAGCAGGAGAATGAAGCCAAATGCCGGAATCAAACCTGGCAAGAA  
 AAAGAATGATTTTGAACAAGGCAATTATATTTGAGAGAAAAGTTGAAAATTCAAATTGAAT  
 CCCTAAGATTATTTAAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCA  
 ACTTTTGGCTATACCCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGA  
 CTATATGCAGAAAATATTCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC  
 CAGTGATTACAAATAGAGCAAGG**TAA**ATGAATACCTTCTGCTGTGCTAGCTATATCGCATC  
 TTAACACTATTTTATTAATTAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGC  
 CACATTTTGGGAGCTTTTCTACATGTCTGTTTCTCATCTGTAAAGTGAAGGAAGTAAACA  
 TGTTTATAAGTAAAAAA



**FIGURE 214**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41221, pI: 8.54, NX(S/T): 0
MYRLLSAVTARAAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGGLGLGLALGVKLAGGLRG
AAPAQSPAAPDPEASPLAEPPEQSLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGA
PGIVVGVSVDGKEVWSEGLGYADVENRVPCPKPETVMRIASISKSLTMVALAKLWEAGKLDLD
IPVQHYVPEFPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN
DPLFFKPGSQFLYSTFGYTLAAIVERASGCKYLDYMQKIFHDLMLTTVQEENEPVIYNRAR
```

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 39-60



**FIGURE 215**

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCG  
 AGGCTGGTGGGAAGAAGCCGAG**ATG**GCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC  
 TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCGGGGAGCGGCTGCCGGGCCGGGACT  
 GGTGCGCGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCTGTGGCAGGTGGGGCTGCT  
 GCTGGAGCACTCATTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCT  
 GGAACCAGCAGGATGGTACCTTGTCCCTGTCACAGCGGCAGCTCAGCGAGGAGAGCGGGGC  
 CGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGG  
 GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGG  
 TGGAGTCGCACCTGTCCGACCAGCTGACCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC  
 GTGTCCGTTGGTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA  
 GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCCACCACAGCCCCAGGCCCTGAGACGGCGG  
 CCTTCATTGAGCGCCTGGAGATGGAACAGGCCCCAGAAGGCCAAGAACCCAGGAGCAGAAG  
 TCCTTCTTCGCCAAATACTGGATGTACATCATTCCCGTCGTCTGTTCTCATGATGTCAGG  
 AGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGGGGTGGGTGGTGGGGGTAGTGGCC  
 TTTGCTGTGTGCCACCCTCCCTG**TAA**GTCTATTTAAAAACATCGACGATACATTGAAATGTG  
 TGAACGTTTTGAAAAGCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGG  
 TCCTGATGTACAAGCTTGATTGAAATCACTGCTCACTTGATACGTTATTCAGAAACCCAAG  
 GAATGGCTGTCCCCATCCTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTAT  
 TAAACTGTCCCCAGATCGACACGCAAAAAAAA

**FIGURE 216**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529

><subunit 1 of 1, 269 aa, 1 stop

><MW: 28004, pI: 5.80, NX(S/T): 1

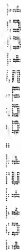
MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI  
DDSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRI PRRP GALDGLEA  
GGYVSSFVPACSLVESHLS DQLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQ  
LQPPTTAPGPETA AFIERLEMEQAQKAKNPQEKSFFAKYWMYIIPVVLFLMMSGAPDTGGQ  
GGGGGGGGGGSGLCVPPSL

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 226-243



**FIGURE 217**

GGAGCGCTGCTGGAACCCGAGCCGAGCCGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCT  
 GGAGCCGGACGTGTCCGGGGCGTCCCGCAGACCGGGGCAGCAGGTGCTCGGGGGGCCACC  
**ATG**CTGGTGACTGCCTACCTTGCTTTTGTAGGCCTCCTGGCCTCCTGCCTGGGGCTGGAAC  
 GTCAAGATGCCGGGTAAACCCCTGGAAGGGCCTGCAGCAATCCCTCCTTCCGTTTC  
 AACTGGACTTCTATCAGGTCTACTTCTGGCCCTGGCAGTGATTGGCTTCAGGCCCCCTAC  
 CTCTATAAATCTACCAGATTACTACTTCTGGAAGGTCAAATTGCCATCCTCTATGTCTG  
 TGGCCTTGCCCTCTACAGTCCCTTTGGCCTAGTGGCCTCCTCCCTTGTGGATTGGCTGGGT  
 GCAAGAATTCTTGTGCTCTTCTCCCTGACTTACTCACTATGCTGCTTAACCAAACCTCTCT  
 CAAGACTACTTTGTGCTGCTAGTGGGGCGAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT  
 CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCCTGCTGAGT  
 GGATCCCAGCTACCTTTGCTCGAGCTGCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT  
 GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGGCCTGTAGCGCCCTTTGTGGCTGC  
 CATCCCTCTCCTGGCTCTGGCAGGGGCCTTGGCCCTTCGAAACTGGGGGGAGAACTATGACC  
 GGCAGCGTGCCCTTCTCAAGGACCTGTGCTGGAGGCCCTGCCTCCTCTGTCGGACCGCCGC  
 GTGCTGCTGCTGGGCACCATACAAGCTCTATTTGAGAGTGTATCTTCATCTTTGTCTTCTCT  
 CTGGACACCTGTGCTGGACCCACACGGGGCCCTCTGGGCATTATCTTCTCCAGCTTCATGG  
 CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG  
 CCCATGCACCTGCTGTCCCTTGCTGTGCTCATCGTCGTCTTCTCTCTTTCATGTTGACTTT  
 CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCTTCATAGCCTTTCTACTTATTGAGT  
 TGGCTTGTGGATTATACTTTCCAGCATGAGCTTCTACGGAGAAAGGTGATCCCTGAGACA  
 GAGCAGGCTGGTGTACTCAACTGGTTCGGGTACCTCTGCACTCACTGGCTTGCCCTAGGGCT  
 CCTTGTCTCCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTACAGCATTTGCTCTG  
 CTGTCATGGTGATGGCTCTGCTGGCAGTGGTGGGACTCTTACCGTGGTAAGGCATGATGCT  
 GAGCTGCGGGTACCTTCACCTACTGAGGAGCCCTATGCCCTGAGCTGT**TAA**CCCCACTCCAG  
 GACAAGATAGCTGGGACAGACTCTTGAATTCAGCTATCCGGGATGTACAGATCTCTCTGT  
 GACTGACTTTGTGACTGTCTGTGGTTTCTCTGCCATTGCTTTGTGTTTGGGAGGACATGA  
 TGGGGGTGATGGACTGGAAGAAGGTGCCAAAAGTTCCTCTCTGTGTTACTCCCATTTAGAAA  
 ATAAACACTTTTAAATGATCAAAAAAAAAA

**FIGURE 218**

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY  
 LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS  
 QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLAVVAG  
 VAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDRR  
 VLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAASLLGSSLYRIATSKRYHLQ  
 PMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFPSMSFLRRKVIPET  
 EQAGVLNWFVRVPLHSLACLGLLVLHDSDRKTGTRNMFSTICSAMVMALLAVVGLFTVVRHDA  
 ELRVPSPTTEEPYAPEL

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,  
 314-330, 343-359, 379-394, 410-430



**FIGURE 219**

GCGACGCGCGCGGGGGCGGCGAGAGGAAACGCGGCGCCGGGCGGGGCCCGCCCTGGAG**ATG**  
 GTCCCCGGCGCGCGGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCCTCGCGGCCCA  
 CGGCTTCCGTATCCATGATTATTTGTACTTTCAGTGCTGAGTCCTGGGGACATTCGATACA  
 TCTTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT  
 CACCTTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAACTCAGCAACGGTTTCTTCATCCA  
 GGACCAGATTGCTCTGGTGGAGAGGGGGGCTGCTCCTTCCTCTCCAAGACTCGGGTGGTCC  
 AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC  
 GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCCTGCTCGG  
 CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT  
 CCATCCAGTCAATGTCAACAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC  
 TGGT**AGA**AAGAGTTTGTCCACATTCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC  
 AGGAATTTTGTACTTGGAAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGA  
 AAAGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCAGG  
 GCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA  
 GAACCCGAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACT  
 CACCTGGCTCCAGCCTCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG  
 AGTGGTTTAAAGAGCTGGTGTGTTGGGGACTCAATAAACCCCTCACTGACTTTTGTAGCAATAAA  
 GCTTCTCATCAGGGTGCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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>>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532
>>subunit 1 of 1, 188 aa, 1 stop
>>MW: 21042, pI: 5.36, NX(S/T): 2
MVPGAAGWCCLVLWLPACVAAHGFRIHIDYLVQVLSPGDIRIYFTTAPKDFGGIFHTRYEQ
IHLVPAEPPEACGLSGNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVVISDNAVNDNSF
VYEMIODSTGTADIPALPFLGRDGMIRSLRLEOHGLPWAIISIPVNVTSIPTFELLQPPWTFW
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amino acids 1-20

**FIGURE 221**

TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCCTGCTGTGTGGGCTGGTGGTGA  
 TGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTG  
 ACTGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAG  
 AGGCCAACCCAAAGATGCCACGGACTGGTGTGCCAGACCCATGACTGCTGCTATGACCACC  
 TGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAGCAGCATACATTGTATGGAT  
 TTATCTCAACGCTATTGTTTAATGGCTGTGTTAATGTGATCTATCTGGAAAATGAGGACTC  
 CGAATAAAAAGCTATTACTAWTTNAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
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**FIGURE 222**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVIFIQGGILNLNKMVKQVTGKMPILSYWPGCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCGIYKDNKSSIHCMDSLQRYCLMAVFNVIYLENEDSE
```

**Important features of the protein:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 1-24

**N-glycosylation site.**

amino acids 86-89

**N-myristoylation sites.**

amino acids 20-25, 45-50

**Phospholipase A2 histidine active site.**

amino acids 63-70

**FIGURE 223**

CTCGCTTCTTCCTTCTGGATGGGGGCCAGGGGGCCCAGGAGAGTATAAAGGCGATGTGGAG  
GGTGCCCGGCACAACCAGACGCCAGTCACAGGCGAGAGCCCTGGGATGCACCGGCCAGAGG  
CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTAT  
GGCCCTGGAGGAGGCAAGTATTTACAGCACCCTGAAGACTACGACCATGAAATCACAGGGCT  
GCGGGTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCCAGGTGAAACTTGAGACTCCTGGG  
ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCTGCAGCCAGGCCAATAC  
ATCACAAAAGTCTTTGTGCGCCTTCCAAGCTTTCTCCGGGGTATGGTCATGTACACCAGCAA  
GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAAG  
AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGC  
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC  
AGCAAACCTACCCGTGGGTGCTTAGGGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT  
GTGGTGGTGGCTGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATA  
AATAAAGCTTCTGCAGAAAA

**FIGURE 224**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVK
LGDSWDVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMYTSKDRYFYFGKLDGQISS
AYPSQEGQVLVGIYGQYQLLGIKISIGFEWNYPLEEPTTEPPVNLTYANSPPVGR
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**Signal peptide:**

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**FIGURE 225**

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCT  
 GAACTGGGTGCTCATCAGCGGAACCTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG  
 CCCCAAATTCCTGGAAGAATACATCATGTTTTTCGATAAGAGAATAATTAGGATCCAGTT  
 TTTTTTTTAAACCGCCCCCTCCCCACCCCCAAAAAACTGTAAGAGTGCAAAAACGTAATAT  
 CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATT  
 TATTTGTTCTTGGAGTGTCTGCGTGGCTGGCAAGAATAATGTTCCAAAATCGGTCCATCT  
 CCAAAGGGGTCCAATTTTTCTTCTCCTGGGTGTGACGAGCCCTGACTCACTACAGTGACGCTG  
 ACAGGGGCTGTATGCAACTGGCCCCTAAGCCAAAGCAAAAGACCTAAGGACGACCTTTGAA  
 CAATACAAAGGATGGGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT  
 ATAGCCCCACTGTCTTACTGACAATGCTTCTTCTGCGGAACGAGGATGCCCTAAGGGCTG  
 TAGGTGTGAAGGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCTCAAGTA  
 TATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCTATAACAGCCTTCAAAAACCTAAGTATAAT  
 CAATTTAAAGGGCTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATAT  
 TGACGAAAATGCTTTTAAATGGAATACGCAGACTCAAAGAGCTGATTCTTAGTTCCAAAGAA  
 TCTCCTATTTTCTTAACAATACCTTCAGACCTGTGACAAATTTACGGAACCTTGGATCTGTCC  
 TATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTCGGGAAGCTGCTGAGTTT  
 ACATTTACGGTCTAACTCCCTGAGAACCATCCCCTGTGCGAATATTCCAAGACTGCCGCAACC  
 TGGAACTTTTGGAGCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTGTCTGGC  
 ATGATCAGACTCAAAGAACCTTCACTGGAGCACAAATCAATTTTCCAAGCTCAACCTGGCCCT  
 TTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCAGTGGAATAAAATCAGTGTATAG  
 GACAGACCATGTCTTGACCTGGAGCTCCTTACAAAGGCTTGATTATCAGGCAATGAGATC  
 GAAGCTTTTCAGTGGACCGAGTGTTCCTCAGTGTGTCGCAATCTGCAGCGCCTCAACCTGGA  
 TTCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACA  
 TCAGTCTTGTGGGAATATATGGGAATGCAGCAGAAATATTGTCTCCCTTGTAACCTGGCTG  
 AAAAGTTTTAAAGGTCTAAGGGAGAATACAATTTATCTGTGCCAGTCCCAAAGAGCTGCAAGG  
 AGTAAATGTGATCGATGCAGTGAAGAATACAGCATCTGTGGCAAAAGTACTACAGAGAGGT  
 TTGATCTGGCCAGGGCTCTCCCAAAGCCGACGTTTAAAGCCAGCTCCCGAGGCCGAAGCAT  
 GAGAGCAAAACCCCTTTGCCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGC  
 TGACGCCGAGCACATCTCTTTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTCTGTCG  
 TGCTCGTCATCTGCTGGTTATCTACGTGTCATGGAAGCGGTACCTGCGAGCATGAAGCAG  
 CTGCAGCAGCGCTCCCTCATGCGAAGGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAAT  
 GACTCCCAGCACCCAGGAATTTTATGTAGATTATAAACCCACCAACCGGAGACCAGCGAGA  
 TGCTGCTGAATGGGACGGGACCTGCACCTATAACAAATCGGGCTCCAGGGAGTGTGAGGTA  
**TGA**ACCATTCTGATAAAAAAGAGCTCTTAAAGCTGGGAAATTAAGTGTGCTTTATTGAACCT  
 TGGTGACTATGAGGAAACGCGATGCCCCCTCCCTTCCCTCTCCCTTCACTTTGGTGG  
 CAAGATCCTTCCCTGTCCGTTTTAGTGCATTATAATACTGGTCATTTTCTCTCATACATA  
 ATCAACCCATTGAATTTAAATACCAATCAATGTGAAGCTTGAACCTCCGGTTTAAATATA  
 TACCTATTGTATAAGACCTTTTACTGATTCCATTAAATGTGCGATTGTTTTAAGATAAAACT  
 TCTTTCATAGGTAATAAAAAAAAAA

**FIGURE 226**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
><subunit 1 of 1, 513 aa, 1 stop
><MW: 58266, pI: 9.84, NX(S/T): 4
MGFNVIRLLSGSAVALVIAPTVLLTMLSSAERGCPKGCRCCEGKMVYCESQKLQEIPSSISAG
CIGLSLRYNQLKLYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRIFQDCRNLELL
DLGYNRIIRSLARNVFAGMIRLKEHLHLEHNQFSKLNALFPRLVSLQONLYLQWNKISVIGQTM
SWTWSSSLQRLDLSGNEIEAFSGPSVFQCVENLQRLNLDNSNKLTFIQEILDSWISLNDISLA
GNIWECSRNICSLVNWLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFFKPKLPRPKHESKPPPLPTVGATEPGPETDADAEHISFHKIIAGSVALFSLVLI
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKRQSLKQMTPTQEFYVDYKPTNTETSEMLLN
GTGPCTYNKSGSRECEV
```

**Important features of the protein:****Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 420-442

**N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

**Tyrosine kinase phosphorylation site.**

amino acids 136-142

**N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

**FIGURE 227**

AGTTCCTGAGAAAGAAGGAAATAAACACAGGCACCAAACTACTATCCTAAGTTGACTGTCCTT  
 TAAATATGTCAGATCCAGACTTTTCAGTGTACCTCAGCGATCTCAACGATAGGGATCTTG  
 TGTTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT  
 AAATTATAATGACCAACACCTTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGG  
 TGGCAGCTCTTCTCTGTGGAGCTGTGGTCCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGA  
 ATTGATTCTCACAGGCGACCATGGCAGTTTTTGGCTGTTGGAGACTTGGACTCTATTTATGG  
 GACAGAAGCAGCTGTGAGTCCAACGTGGGAATTCACCTTCAAACCTCAAACCCCTGACCTAT  
 ATCCTGTTCTCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTTGTA  
 AAAACAACCTGATTTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTTCCA  
 AAACATCAAAATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTATATA  
 GTCTGAGGAAGGACAATTCGACAAAAAGATGGATGTTGGAAAAAATTTTGGTCATGGAGATG  
 TTTAAATAGTAAAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACAC  
 AACCAAATTAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT  
 TCCATCACATTTAGGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTC  
 CTAGCATGGGGTCCATAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAAATCCAACAT  
 GTCCAGAACCAGAACCAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA  
 GAAAAGTTTGGAGTTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT  
 CAGCAAAAACAAGAGGTTTTATGCCCAACCTGAAGAGGAAGAAATGTAGATAGAAGGTGA  
 AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC  
 CTTTTACAGTAATGAATGTGGCTCCATAGTCCATAGTGTCTCTGAGGCTCAGGGCTTG  
 GCATTTATTGCAGCATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC  
 AGAAGTAGCAATGAGACATCTTCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGA  
 CAAAACATCCATCACAGATGACATATGATCTTCAGCTGACAAATTTGTTGAACAAAAACAAT  
 AAACATCAATAGATATCTAAAAA

**FIGURE 228**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSIAISTIGILCLPLFQLVLSLDLPCEEDEMVCVNYNDQHPNGWYIWILLLLVLVA  
ALLCGAVVLCLQCWLRPRIDSHRRTMVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP  
VPAPCFGPLGSPPPYEIVKTT

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 52-70

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**FIGURE 229**

GAGCGGAGTAAAACTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGT  
 TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGAGCGAGCTGAGCGCCCGCTTATTA  
 GCTCTCGCTGCGTCGCCCGGGCTCAGAAGCTCCGTGGCGGGCGGACCGTGACGAGAGAAGCC  
 ACGGCCAGCTCAGTTCCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTTAAACT  
 CCCTCTTCAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAG  
 ATGAAGAATATACAATATTGAGGATATTTTTTTCTTTTTTTTCAAGTCTTGATTTGTGGC  
 TTACCTCAAGTTACCATTTCAGTCAAGTCTGTTTGTGCTTCTTCAGAAATGTTTTTTA  
 CAATCTCAAGAAAAAATATGTCCAGAAATTGAGTTTACTGTTGCTTGATTTTGGACTCATT  
 TGGGGATTGATGTTACTGCACATATACTTTCAACAACCAAGACATCAAGCAGTGTCAAGTT  
 ACGTGAGCAAACTACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAAATAAGA  
 ACACAGTGGATGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAATT  
 GCTGTCCCTCTGGATGACATTTTGAACAGATTGGTGAAGCTGGAGAACAAGTTGACTATAT  
 TGTGTGAATGGCTCAGCAGCCAAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAA  
 CCACAAATAAAGAAGCAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAAATCACCTTGTGC  
 TGCTCCATCCACTGTGGATTATATCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGAC  
 AGAGCAATACCTTTACAATAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTTCATGGAAC  
 TCTAATCTGTACATAAAAAATTTTAAAGTTATTTGTTTGCCTTCAGGCAAGTCTGTTCAATG  
 CTGTACTATGTCTTAAAGAGAATTTGGTAACTTGGTTGATGTGGTAAGCAGATAGGTGAGT  
 TTTGTATAAATCTTTTGTGTTTGAGATCAAGCTGAAATGAAACACTGAAAACTGGATTCT  
 ATTTCTATAACACATTTATTTAAGTATATAACACGTTTTTTGGACAAGTGGAAGATGTTTAA  
 TCATTCTGTCATTTGTTCTCAATAGATGTAACCTGTTAGACTACGGCTATTTGAAAAATGTG  
 CTTATTGTACTATATTTTGTATTCCAATTATGAGCAGAGAAAGGAATATAATGTTGAAAA  
 TAATGTTTTGAAATCATGACCCAAGAATGTATTGATTTGCACTATCCTTCAGAAATACTGA  
 AGGTTAATATTATGTATATTTTAAAAATTACACTTATAAGAGTATAATCTTGAATGGGTAG  
 CAGCCACTGTCCATTACCTATCGTAAACATTGGGGCAATTTAATAACAGCATTAAAAATAGTT  
 GTAAACTCTAATCTTATACTTATTGAAGAATAAAGATATTTTATGATGAGAGTAACAATA  
 AAGTATTATGATTTTTCATACATGATGAATGTTCAATTTAAAGTTAATCCTTTGAGTGTCT  
 ATGCTATCAGGAAGGCACATTATTTCATATTTGGGTAAATTTGCTTTTATTATATTGGTC  
 TAGGAGGAAGGGACTTTGGAGAATGGAACCTTGAGGACTTTAGCCAGGTGTATATAATAAA  
 GGTACTTTTGTGCTGCATTAAATTGCTTGGAAAGTGTTAAACATTATATTATATAAGAGTATC  
 CTTATGAAATTTTGAATTTGTATAACAGATGCATTAGATATTCATTTTATATAATGGCCAC  
 TTAANAATAAGAACATTTAAAAATATAAACTATGAAGATTGACTATCTTTTCAGGAAAAAAGCT  
 GTATATAGCACAGGGAACCCCTAATCTTGGGTAATCTAGTATAAAAACAAATATACTTTTAT  
 TTAATTTTCCCTTTGTAGCAAACTTAATTGCCACATGGTGGCCCTATATTTTCATAGTATTTAT  
 CTCATAGTAACCTGCTTAAGTGCAGCTAGCTTCTAGATTTAGACTATAGAAATTTAGATAT  
 TGTATTGTTGCTCATTATAATATGCTACCACATGTAGCAATAATTACAATATTTTATTAAAA  
 TAAATATGTGAAATATTTGTTTCATGAAAGACAGATTTCCAAATCTCTCTCTCTCTCTGTA  
 CTGTCTACCTTTATGTGAAGAAATTAATTATATGCCATTGCCAGGT



**FIGURE 230**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL
VPVTTNKRTNVSGSIR
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**Important features of the protein:****Signal peptide:**

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**FIGURE 231**

CGCGGCCGGGCCCGGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAGGCTTCCAGCCCCAC  
**CATG**CCGTGGCCCCCTGCTGCTGCTGCTGGCCGTGAGTGGGGCCAGACAACCCGGCCATGCT  
TCCCCGGGTGCCAATGCGAGGTGGAGACCTTCGGCCTTTTCGACAGACTTCAGCTGACTCGG  
GTGGATTGTAGCGGCCCTGGGCCCCACACATCATGCCGTTGCCCATCCCTCTGGACACAGCCCA  
CTTGGACCTGTCTCCAACCGGCTGGAGATGGTGAATGAGTCGGTGTTGGCGGGGCGGGGT  
ACACGACGTTGGCTGGCTGGATCTCAGCCACAACCTGCTCACCAGCATCTCACCACCTGCC  
TTCTCCCGCCTTCGCTACCTGGAGTCGCTTGACCTCAGCCACAATGGCCTGACAGCCCTGCC  
AGCCGAGAGCTTCACCAAGCTCACCCTGAGCGACGTGAACCTTAGCCACAACCAAGCTCCGGG  
AGGTCTCAGTGTCTGCCTTCACGACGCACAGTCAGGGCCGGGCACTACACGTGGACCTCTCC  
CACAACCTCATTACCGCCTCGTGCCCCACCCACGAGGGCGCGGCTGCCTGCGCCACCATT  
TCAGAGCCTGAACCTGGCCTGGAAACCGGCTCCATGCCGTGCCAACCTCCGAGACTTGCCCC  
TGCGCTACCTGAGCCTGGATGGGAACCTCTAGCTGTATTGGTCCGGGTGCCTTCGCGGGG  
CTGGGAGGCTTACACACCTGTCTCTGGCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCAG  
TGGCTTCCTCGTGAGCTACCGGGCCTGCAGGTCTCGGCAACCCCAAGCTTAACT  
GGGCAGGAGCTGAGGTGTTTTCAGGCCTGAGCTCCCTGCAGGAGCTGGACCTTTCGGGCACC  
AACCTGGTGCCCTGCCTGAGGCGCTGTCTCTCCACCTCCCGGCATCGAGAGCGTCAGCGT  
GGGCGAGGATGTGCGGTGCGCGCGCTGGTGCGGGAGGGCACCTACCCCGGAGGCTGGCT  
CCAGCCCCAAGGTGCCCTGCACTGCGTAGACACCCGGGAATCTGCTGCCAGGGGCCCCACC  
ATCTT**TGA**CAATGGTGTGGCCCAGGGCCACATAACAGACTGCTGTCTGGGCTGCCTCAG  
TCCCGAGTAACCTTATGTTCAATGTGCCAACACCAAGTGGGGAGCCCGCAGGCTTATGGGA  
GCGTCACCAACAGGAGTTGTGGGCTTAGGAGAGGCTTTGGACCTGGGAGCCACACCTAGGAGC  
AAAGTCTCACCCTTTGTCTACGTTGCTTCCCAAACCATGACGAGGGGACTTCGATGCCA  
AACCAGACTCGGGTCCCCCTCTGCTTCCCTTCCCCACTTATCCCCAAGTGCCTTCCCTCAT  
GCCTGGGCGCGCTGACCCGCAATGGGCGAGAGGTGGGTGGGACCCCTGCTGCAGGGCAGA  
GTTCAGGTCCACTGGGCTGAGTGTCCCTTGGGCCCATGGCCCACTCACTCAGGGGCGAGTT  
TCTTTTCTAACATAGCCCTTCTTTGCCATGAGGCCATGAGGCCCGCTTCATCCTTTTCTAT  
TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAAGAATCAAGTCCACCTTCTCATGTGAC  
AGATGGGGAACCTGAGGCCTTGAGAAGGAAAAAGGCTAATCTAAGTTCCTGCGGGCAGTGGC  
ATGACTGGAGCACAGCCTCTGCCTCCAGCCCGGACCCAAATGCACCTTTCTTGCTCTCTTA  
ATAAGCCCCACCTCCCCCGCTGGGCTCCCTTGCTGCCCTTGCTGTTCCCATTAGCACA  
GGAGTAGCAGCAGCAGGACAGGCAAGAGCCTCACAAGTGGGACTCTGGGCCTCTGACCAGCT  
GTGGCGCATGGGCTAAGTCACTCTGCCCTTCGGAGCCTCTGGAAGCTTAGGGCACATTGGTT  
CCAGCTAGCCAGTTTCTCACCTGGGTGGGGTCCCCAGCATCCAGACTGGAAACCTACC  
CATTTTCCCCTGAGCATCCTCTAGATGCTGCCCAAGGAGTGTCTGACGTTCTGGAGCCTACA  
TCTGGCTGGGATCTCAAGGGCCCTCCTGGATTCACTCCCACTGGCCTGAGCAGCAGCAGC  
CCTTCTTACCCTCCCAGGAATGCCGTGAAGGAGACAAGGTCTGCCGACCCATGTCTATGC  
TCTACCCCCAGGGCAGCATCTCAGCTTCCGAACCTGGGCTGTTTCTTAGTCTTCAATTTTA  
TAAAGTTGTTGCTTTTAAACGAGTGCTCACTTCAACCGGCTCCCTACCCCTGCTGGC  
CGGGATGGAGACATGTCATTGTAAAGCAGAAAAAGGTTGCATTGTTCACCTTTTGTAAT  
ATTGTCCTGGGCTGTGTTGGGGTGTGGGGGAAGCTGGGCATCAGTGGCCACATGGGCATC  
AGGGGCTGGCCCCACAGAGACCCACAGGCGAGTGAGCTGTGCTTCCCCACCTGCCCTAGC  
CCATCATCTATCTAACCGGTCTTGATTTAATAAACCTATAAAAGGTTTAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 232**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652
><subunit 1 of 1, 353 aa, 1 stop
><MW: 37847, pI: 6.80, NX(S/T): 2
MPWPLLLLLAVSGAQTRPCFPQCCEVETFGFLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLLDSHNGLTALP
AESFTSSPLSDVNLNSHNQLREVSVSAFTTHSQGRALHVDLSHNLIHRLVPHPTRAGLPAPTI
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAAGLGLTHLSLASLQRLPELAPS
GFRELPGQLQVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVLPEALLLHLPALQSVSV
GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL
```

**Signal peptide:**

amino acids 1-16

**Transmembrane domains:**

amino acids 215-232, 287-304

**FIGURE 233**

GATGGCGCAGCCACAGCTTCTGTGAGATTCGATTTCTCCCCAGTTCCTGTGGGTCTGAGG  
 GGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTAT**ATG**CGTCAATTCCCCA  
 AAACAAGTTTTGACATTTCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCTGT  
 GTTCCAGGCCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC  
 CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTTCTTTCAC  
 GGGAGGCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTCAAGCCTAAGATGAAAGCC  
 TCTAGTCTTGCCCTCAGCCTTCTCTGTCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG  
 ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATG  
 GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAACATTGACATCAGAATCTTA  
 AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT  
 GCTAAGACTCTATCTGGACAGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCC  
 GGAAGATCAGCAGCCTCGCCAATTCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT  
 GCCACATGACATGCCATTGTGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA  
 CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAAGTACAGATTCTTC  
 TGCAATGGATGGAGGAGACAGAA**TAG**GAGGAAAGTGATGCTGCTGTCTAAGAATATTCGAGGT  
 CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCAAACCACCATCTCTTTACT  
 GTACTAGTCTTGTGCTGGTCAAGTGATCTTATTTATGCATTACTTGCTTCCTTGCATGAT  
 TGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGATAAGATTTTGTAAATATCTT  
 TCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTGTCTATTTAATGTATTT  
 ATTTTTTTACTTGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAG  
 AGCAGGTGATGTATTTTATACAGTAAAAAATAACCTTGTAATTTCTAGAAGAGTGGCT  
 AGGGGGTTATTCATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA  
 TATTTGAAATGAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTTGTGTGGAATT  
 GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAAATTGTGTAT  
 CTTCAGCCAGGAATCTTACAGGCCAGCATGTATTTCTACAAATAAAGTTTCTTTGCATA  
 CCAAAAAAAAAAAAAAAAAA

**FIGURE 234**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPG LTCWALTAEPGWGQNKGATTCATNSHSDSELRP
EIFSSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLD RVFKNYQTP
DHYTLRKISSLANSF LTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQA AAVVKALG
ELDILLQWMEETE
```

**Important features of the protein:****Signal peptide:**

amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 192-195, 225-228

**N-myristoylation sites.**

amino acids 42-47, 46-51, 136-141

**FIGURE 235**

CCGTTATCGTCTTGCGCTACTGCTGA**ATGT**CCGTCCCGGAGGAGGAGGAGAGGGCTTTTGCCG  
 CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGC  
 CGAGCTAGCAACCTTTCCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAG  
 CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACA  
 GCCCTAGGGATCATTGAAGAGGAAGGCTTTCTA**AAGCT**TGGCAAGGAGTGACACCCGCCAT  
 TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTG  
 TGTTTGGCAAAAGTGAAGATGAGCATTATCCCCTTTGAAATCAGTCATTGGAGGGATGATG  
 GCTGGTGTTATTGGCCAGTTTTTAGCCAATCCAACTGACCTAGTGAAGGTTTCAGATGCAAAT  
 GGAAGGAAAAAGGAACTGGAAGGAAAACCAATTGCGATTTTCGTGGTGACATCATGCATTTG  
 CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCCAATATACAA  
 AGAGCAGCACTGGTGAATATGGGAGATTTAACCCTTATGATACAGTGAAACACTACTTGGT  
 ATTGAATACACCACTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGAC  
 TGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCATCAAAGCAGAATAATGAATCAACCA  
 CGAGATAACAAGGAAGGGGACTTTTGTATAAATCATCGACTGACTGCTTGATTCAAGGCTGT  
 TCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTACCATCTTGGCTGAGAATGACCC  
 CTTGGTCAATGGTGTTCTGGCTTACTTATGAAAAAATCAGAGAGATGAGTGGAGTCAGTCCA  
 TTT**TAA**

**FIGURE 236**

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568
><subunit 1 of 1, 323 aa, 1 stop
><MW: 36064, pI: 9.33, NX(S/T): 1
MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDA
RESAPYRGMVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLREVVFVGKSEDEH
YPLWKSIVIGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHHAFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVNLTPLEDNIMTHGLSSLCISGLVASILGTP
ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTFPWSMVFWLT
YEKIREMSGVSPF

```

**Transmembrane domains:**

amino acids 25-38, 130-147, 233-248

**FIGURE 237**

CGGACGCGTGGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGC  
 GCCTGAAGTCGCGTGGGCGTTTGAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGC  
 TTAAGAAGTAAAAATGGCAGGCTTCCTAGATAATTTTCGTTGGCCAGAATGTGAATGTATTG  
 ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTCGCAGGTATATTGTTTTTACAGGC  
 TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGAACCATGCGCTT  
 TCACACATGTGGTGTATTTTCCACATTGGCTTTCTTCATGATAAATGCTGTATCCAATGCTC  
 AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGCGCTT  
 TTCATTGGTTTCATGTGTATGTTGGGTCACTTATTGCTCCATGTGGATTCTTTTTGGTGC  
 ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTCAAATGCACCTTA  
 TATTTTTAGCACTCTGATCTACAAATTTGGAAGAACCGAAGAGCTATGGACCTGAGATCAC  
 TTCTTAAGTCACATTTTCCTTTTGTTATATTCTGTTGTAGATAGTTTTTTATCTCTCAGT  
 ACACATTGCCAAATGGAGTAGATTGTACATTAATGTTTTGTTTCTTTACATTTTTATGTTT  
 TGAGTTTTGAAATAGTTTTATGAAATTTCTTTATTTTTTCATTGCATAGACTGTTAATATGTA  
 TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTTATTCCTGAGATTTAGAA  
 CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCATTTTAGAAGTAACCACTCTTGT  
 CTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGG  
 CCGATTGCTTGAGGTCAAGTGTGTTGAGACCGCCTGGCCAACATGGCGAAACCCCATCTACT  
 AAAAATACAAAATTAGCCAGGCATGGTGGTGGGTGCGCTGTAATCCAGCTACCTGGGAGGC  
 TGAGGCAGGAGAATCGCTTGAACCCGGGGGCGAGAGGTGCGAGTGAGCTGAGTTTGCGCCAC  
 TGCACCTCTAGCCTGGGGGAGAAAGTGAACTCCCTCTCAAAAAAAGACCACTCTCAGTATC  
 TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA  
 TAAAGGTTTTGAGCAAGTTGTAACCTATTTTGGCCTAAAAATGAGGTTTTTTTGGTAAAGA  
 AAAAATATTTGTTCTTATGTATTGAAGAAGTGACTTTTATATAATGATTTTTTAAATGCC  
 AAAGGACTAGTTTGAAGGCTCTTTTAAAAAGAATTCCTCTAATATGACTTTTATGTGAGAA



**FIGURE 238**

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWIMIDAADVYPKPEQLNHAFHTCG  
 VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ  
 NTDVYPGLAVFFQNALIFFSTLIYKFGRTTELWT

**Important features:****Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 23-42 (type II), 60-80, 97-117, 128-148

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**FIGURE 239**

GTTGATGGCAAACCTTCTCAAAGGAGGGGCAGAGCCTGCCAGGGCAGGAGCAGCTGGCCCA  
 CTGGCGGCCCCGCAACACTCCGTCTCACCCCTCTGGGCCACTGCATCTAGAGGAGGGCCGTCT  
 GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTGAGAAGCTGGCCAGGGTGGT  
 GGTGAGCTGGGTGAGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG  
 GGAAGTGGGAGCCTCGAGCCCTCGGGTGAAGCTGACCCCAAGCCACCCTTCACTGGACAG  
**GATG**AGAGTGTGAGGTGTGCTTCGCCCTCTGGCCCTCATCTTTGCCATAGTCACGACATGGA  
 TGTATTATTCGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA  
 GCCTCGCCCACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCC  
 AGCCAACTACTTTGCGTTTTAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGT  
 GCTTTGAAGACCGCATGATCATGAGTCCTGTGAAAAACAATGTGGGCAGAGGCCTAAACATC  
 GCCCTGGTGAATGGAACACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG  
 AGATGTTATGCACCTAGTGAAATTCTTTAAAGAAATTCGGGGGGTGCCTGGTGTGGTGG  
 CCTCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAACTCTTCTGACTTG  
 GGGAGTTCCTACGCAAAACAACCTGGGCTTCGGGACAGCTGGGTCTTCATAGGAGCCAAAGA  
 CCTCAGGGGTAAAAAGCCCTTTGAGCAGTTCTTAAAGAACAGCCAGACACAACAATACG  
 AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCGAAGCCATTT**TAG**GGTGGC  
 TGTGGCTCTTCTCAGCCAGGGGCCCTGAAGAAGCTCTGCCTGACTTAGGAGTCAGAGCCCG  
 GCAGGGGCTGAGGAGGAGGAGCAGGGGGTGTGCGTGAAGGTGCTGCAGGTCTTGACGCG  
 TGTGTGCGCCTCTCTCTCGGAAACAGAACCTCCACAGCACATCCTACCCGGAAGACC  
 AGCCTCAGAGGGTCTTCTGGAACAGCTGTCTGTGGAGAGAATGGGGTGTCTTCGTCAGG  
 ACTGTGACGGCTGGTCTGAGGAAGGACAACTGCCAGACTTGAGCCCAATTAAATTTTA  
 TTTTTGCTGGTTTTGAAAAAAAAAAAAAAAAAAAA

**FIGURE 240**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24963, pI: 9.64, NX(S/T): 1

MRVSGVLRLLALIFAIVTTWMFIRSYMFSMKTIRLPWLAASPTKEIQVKKYKCGLIKPCP  
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG  
DVMHLVKFLKEIPGGALVLVASYYDDPGTKMNDESRLKFSDLGSSYAKQLGFRDSWVFIGAKD  
LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

**Important features:****Signal peptide:**

amino acids 1-15

**ATP/GTP-binding site motif A (P-loop).**

amino acids 184-191

**N-glycosylation site.**

amino acids 107-110

**FIGURE 241**

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGGAT  
 CCAGAAACCCATGATACCCTACTGAACACCGAATCCCTGGGAAGCCCACAGAGACAGAGACA  
 GCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTC  
 TCACTCCTCCCTCCCTCTCTCTCTGCTGTCTAGTCCTCTAGTCCTCAAATCCCAGTCCC  
 CTGCAACCCCTTCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTGGATCC  
 TGGCTGCAGATGGGGTCAACACTGGACGTATGAGGGCCACATGGTCAGGACCATTGGCCA  
 GCCTCTTACCCTGAGTGTGGAACAATGCCAGTCGCCCATCGATATTCAGACAGACAGTGT  
 GACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCAGC  
 CTTTGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTTACCTGTATCTG  
 GGTGGACTTCCCCAAAAATATGTAGCTGCCAGCTCCACCTGCATGGGGTCAGAAAGGATC  
 CCCAGGGGGTCAAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTAC  
 ATTATGACTCTGATTCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCCTCAGGGCCTGGCT  
 GTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG  
 TCACTTGACATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTCAACCTAAGAG  
 AGCTGCTCCCCAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACTCCCCCT  
 TGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGGTCCCAGATTTCAATGGAACAGCT  
 GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGA  
 ACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTCTTTCATCCAAGCAGGA  
 TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTG  
 CCTTCTCCTGGCTGTTTATTTTCATTGCTAGAAAGATTCCGAAGAAGAGGCTGGAAAACCGAA  
 AGAGTGTGGTCTTCACCTCAGCACAAAGCCACGACTGAGGCATTAAATTCCTTCTCAGATACCA  
 TGGATGTGGATGACTTCCTTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTG  
 GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCTCCTTCCCCTGGACATCTCTTAGAGAG  
 GAATGGACCCAGGCTGTCAATCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTA  
 GGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGANCAAACCTCTGTTAGTTGCAGGG  
 GAAGTTTGGGATATACCCCAAAGTCCTCTACCCCTCACTTTTATGGCCCTTTCCTAGATA  
 TACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTGTATCAATA  
 TATTGGAAATTAAGTTTCTGACTTT

**FIGURE 242**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWFPASYPECGNNAQSPIDIQTDSVTFDPLP
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQ
INSEATFAELHIVHYDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTI
FSTEEEPSKLLVQNYRALQPLNQRMVFASFQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF
IARKIRKKRLENRKSVMFTSAQATTEA
```

**Important features of the protein:****Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

[illegible]

**FIGURE 244**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGLTPNQQQSNQVFPSSLISLIPLTQM  
 LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGGLNVQQQLHPHVLPIFVTQLGAQGTILSSEE  
 LPQIFTSLLIHSLEFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTTPAGRLPTPSG  
 TDDDFAVTTFAGIQRSTHAIEEATTESANGIQ

**Signal peptide:**

amino acids 1-16

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**FIGURE 245**

GGAGAGAGGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCCTCGGAGCGCGGCG  
 GAGCCAGACGCTGACCACGTTCTCTCCTCGGTCTCCTCCGCTCCAGCTCCGCGCTGCCCG  
 GCAGCCGGGAGCC**ATG**CGACCCAGGGCCCCGCGCCTCCCGCAGCGGCTCCGCGGCTCC  
 TGCTGCTCCTGCTGCTGCAGTGTCCCGCGCCGTGAGCGCCTCTGAGATCCCCAAGGGAAG  
 CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG  
 GCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCGGGTACACCTG  
 GGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGAATGTCTGAGGGAAAGCTTTGAG  
 GAGTCTGGACACCCAACCTACAAGCAGTGTTCATGGAGTTCATTGAATTATGGCATAGATCT  
 TGGGAAAATTGCGGAGTGATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT  
 TCAGTGGCTCACTTCGGCTAAAAATGCAGAAATGCATGCTGTGAGCGTTGGTATTTACATTCT  
 AATGGAGCTGAATGTTTCAAGACCTCTTCCATTGAAGCTATAATTTATTTGGACCAAGGAAG  
 CCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAG  
 GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTGGCACTTGTTTCAAGATTACCCAAAA  
 GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAA**TA**  
**AA**TGCTTTAATTTTCATTGTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAAT  
 GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAGCAAAGCTAAATATGTTTACAGA  
 CCAAAGTGTGATTTACACAGTGTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAGT  
 GGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTA  
 TAATTTGGAATATTTGTGTGCTTTTTTTTTTCTCTTAGTATAGCATTTTTTAAAAAATA  
 TAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAAT  
 AAAAATTATTTCCAACA



**FIGURE 246**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGFAASPQRLRGLLLLLLLQLPAPSSASEIPK GKQKAQLRQREVVDLYNGMCLQGPA  
PGRDGSPGANVIPGTPGIPGRDGFKEGEGCLRESFEESWTFPNYKQCSWSSLNYGIDLGKIA  
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYYLDQGSPEMN  
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217